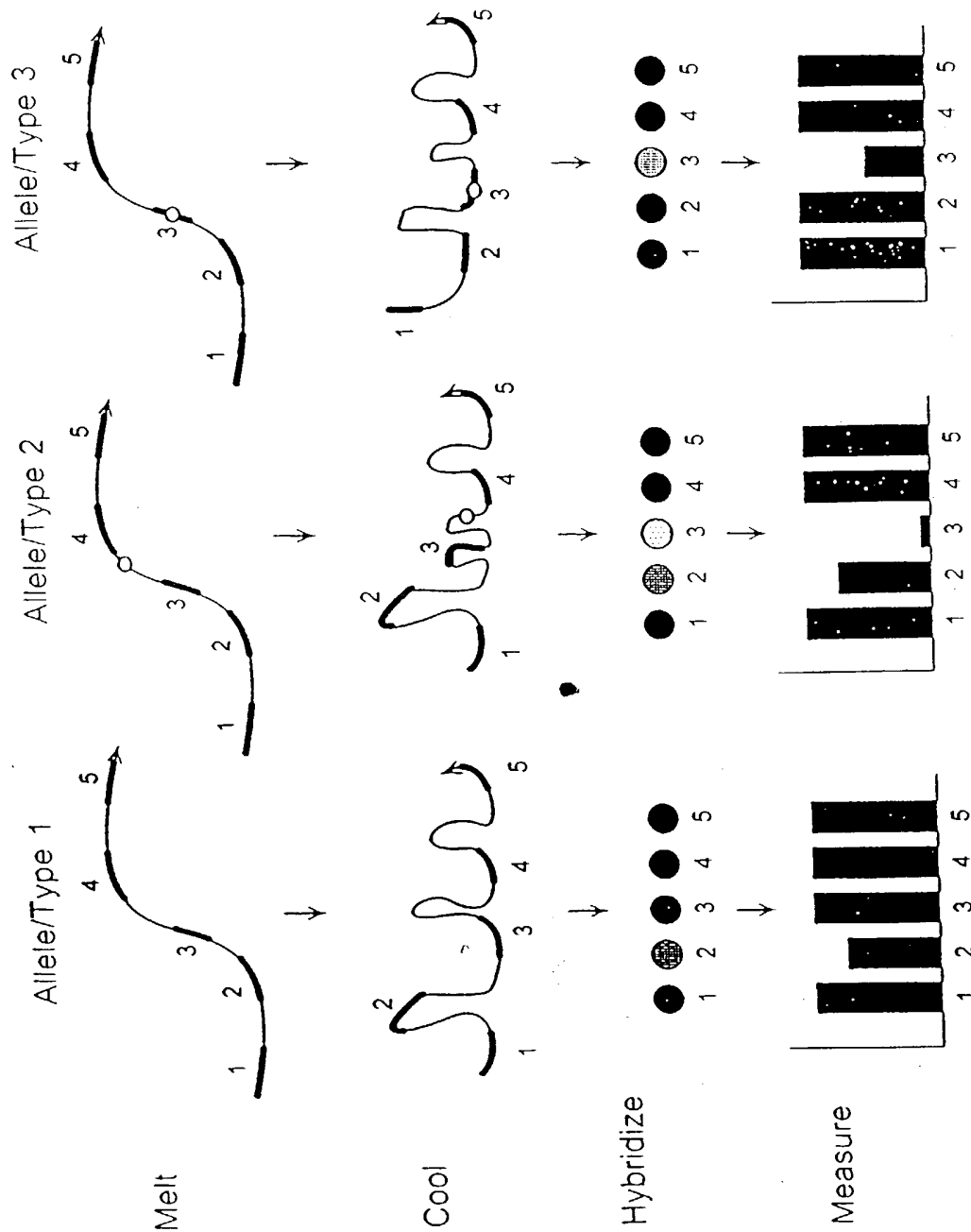


FIGURE 1



8/123

FIGURE 2

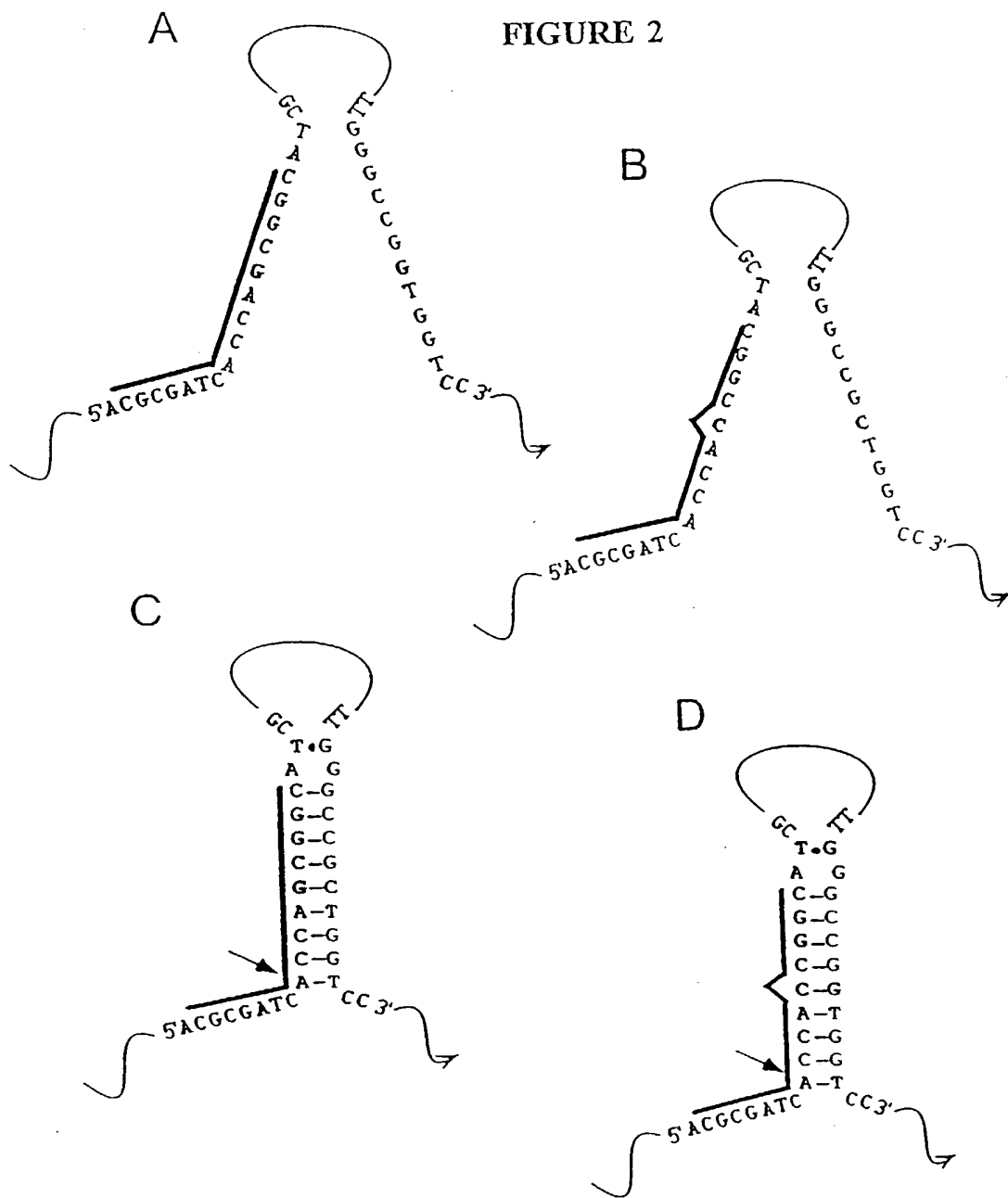


FIGURE 3

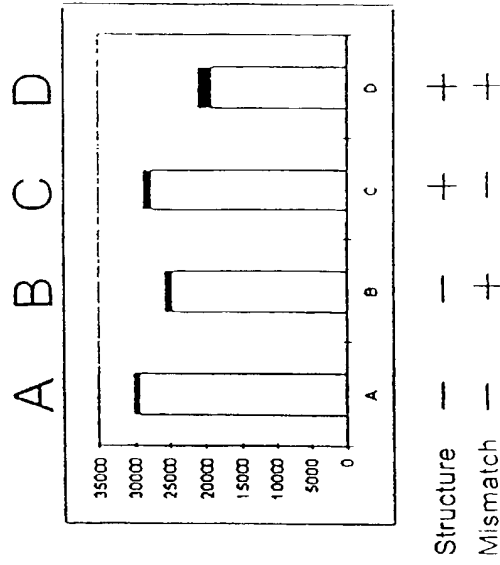
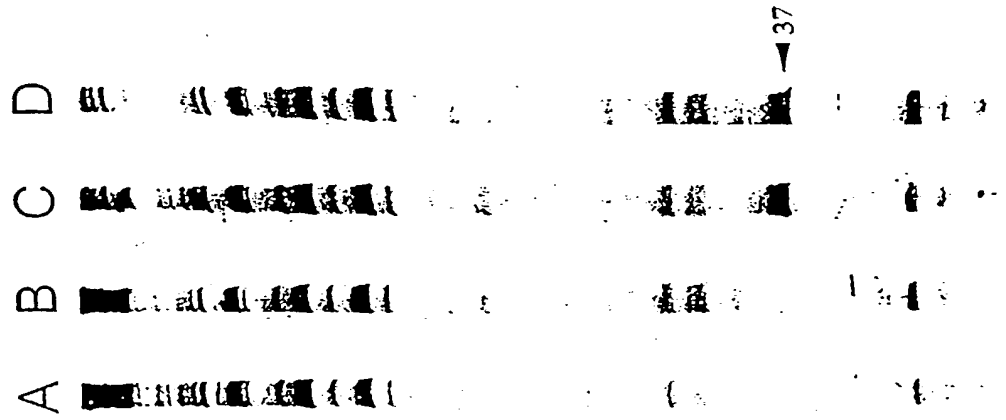
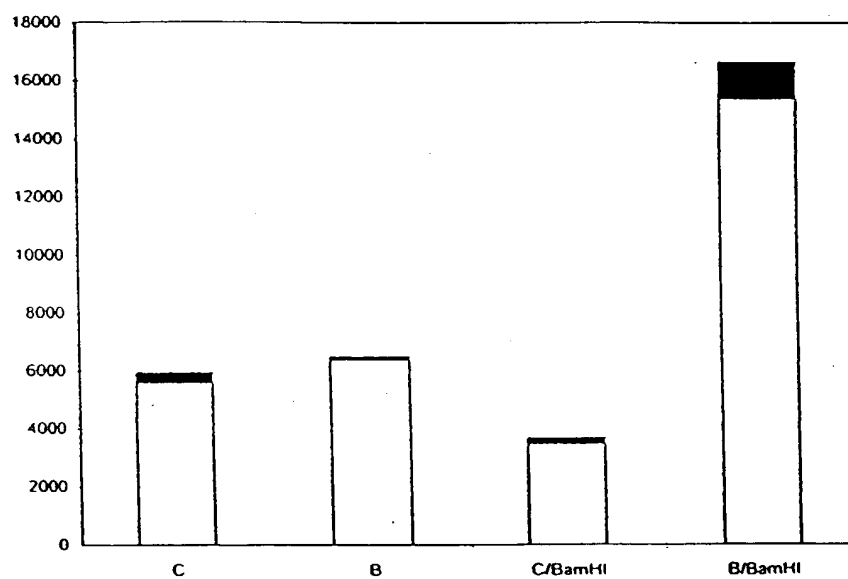


FIGURE 4



4/123

FIGURE 5

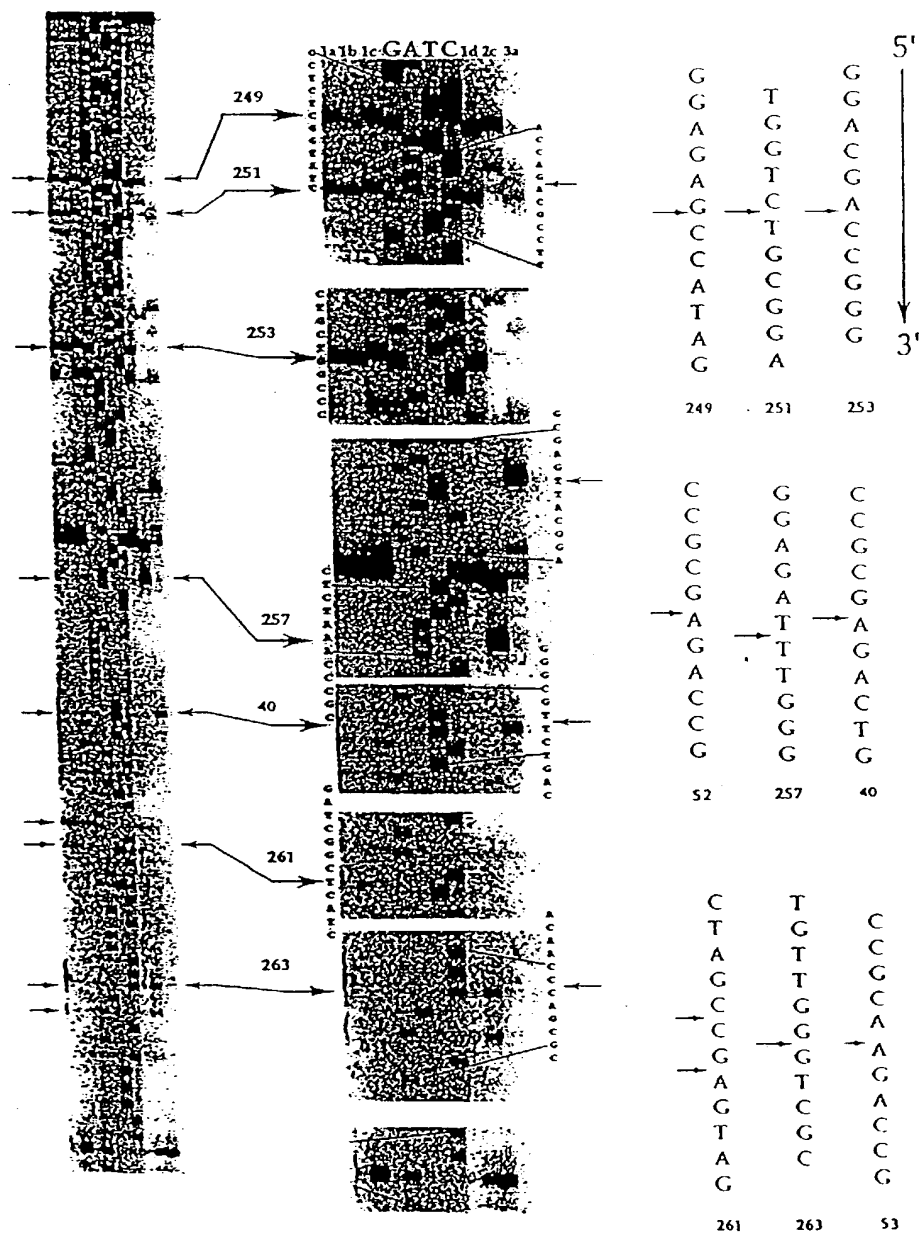


FIGURE 6

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|
| Consensus: | GATTCTGTCT | TCACGCAGAA | AGCGTCTAGC | CATGGCGTTA | GTATGAGTGT | CGTGCAGCCT |
| HCV 1a | ----- | ----- | ----- | ----- | ----- | ----- |
| HCV 1b | ----- | ----- | ----- | ----- | ----- | ----- |
| HCV 2c | ----- | ----- | ----- | ----- | ----- | -A----- |
| HCV 3a | ----- | ----- | -C----- | ----- | -C----- | ----- |

| | | |
|------------|------------|------------|
| | #249 | #251 |
| CCAGGACCCC | CCCTCCCGGG | AGAGCCATAG |
| ----- | ----- | TGGTCTGCGG |
| ----- | ----- | AACCGGTGAG |
| ----- | ----- | TACACCGGAA |
| ----- | ----- | ----- |
| -T----- | ----- | ----- |
| ----- | ----- | ----- |
| -C----- | ----- | ----- |
| ----- | -A----- | ----- |

| | |
|--------------|----------------|
| #253 | #257 |
| TTGCCAGGAC | GACCGGGTCC |
| ----- | TTTCTTGAT |
| ----- | CAACCGCTC |
| ----- | AATGCCCTGA |
| ----- | GATTGGGCG |
| ----- | ----- |
| ----- | ----- |
| -G--A--T-- | A--A--T-- |
| -C--TG--GT-- | -G--A--CA--A-- |

| | | |
|------------|------------|------------|
| #40 | #261 | #263 |
| TGCCCCCGCA | AGACTGCTAG | CCGAGTAGTG |
| ----- | ----- | TTGGGTGCGG |
| ----- | ----- | AAAGGCCTTG |
| ----- | ----- | TGGTACTGCC |
| ----- | ----- | ----- |
| -G----- | ----- | ----- |
| ----- | -C----- | -T----- |
| -G----- | -TCA-- | ----- |

| | | | | |
|------------|------------|------------|------------|-----------|
| TGATAGGGTG | CTTGGGAGTG | CCCCGGGAGG | TCTCGTAGAC | CGTGCAATC |
| ----- | ----- | ----- | ----- | ----- |
| ----- | ----- | ----- | ----- | ----- |
| ----- | -A----- | ----- | ----- | ----- |
| ----- | ----- | ----- | ----- | ----- |

FIGURE 7

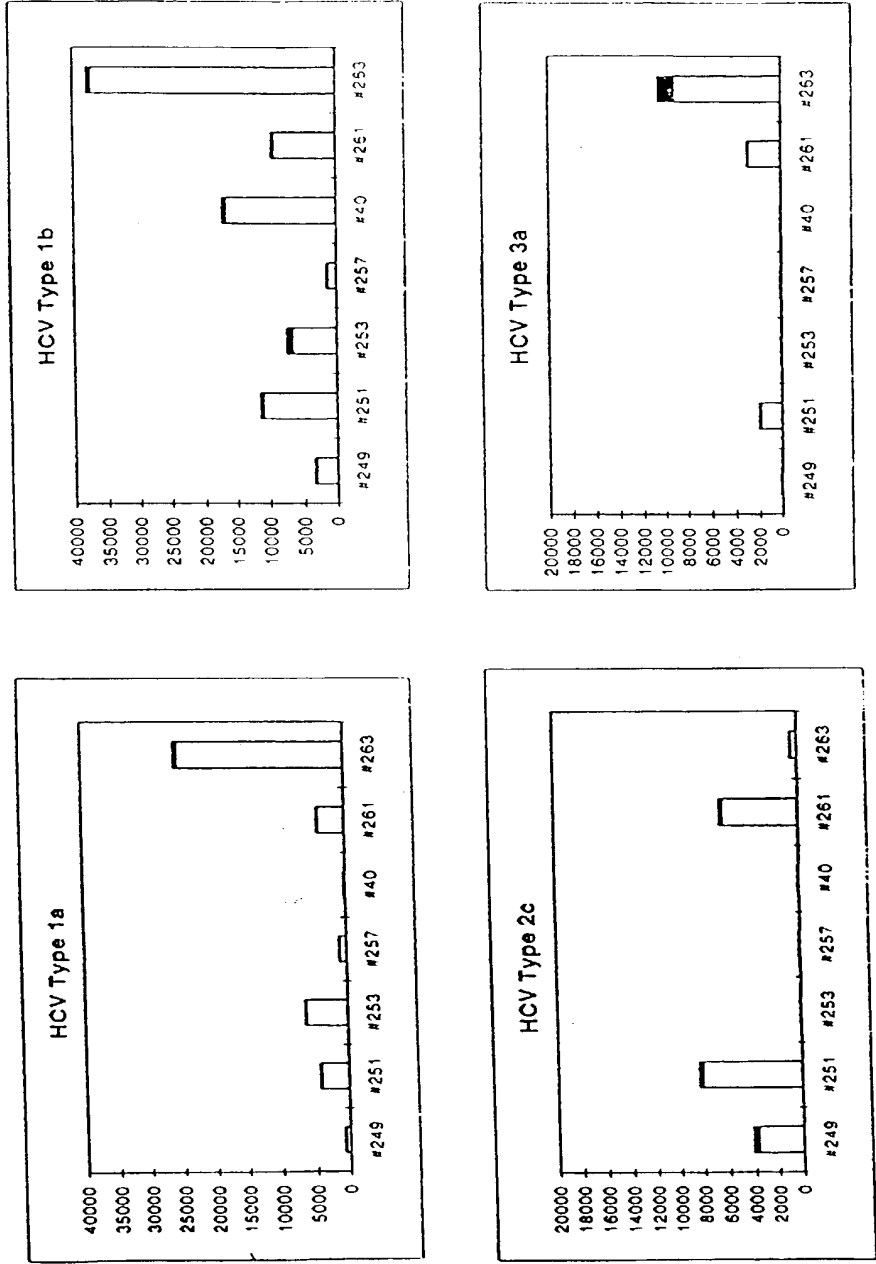
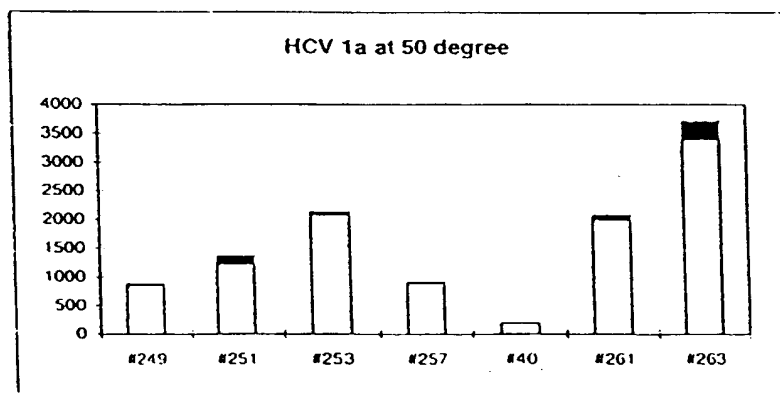
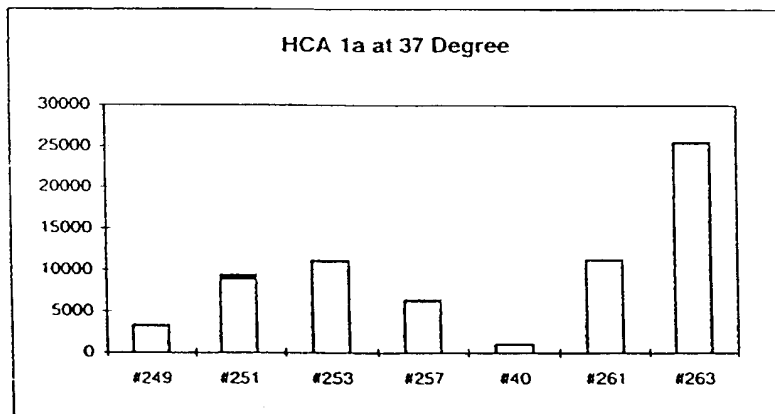
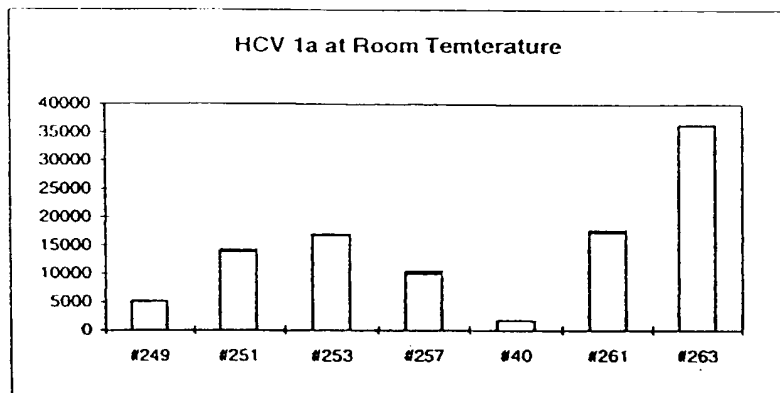
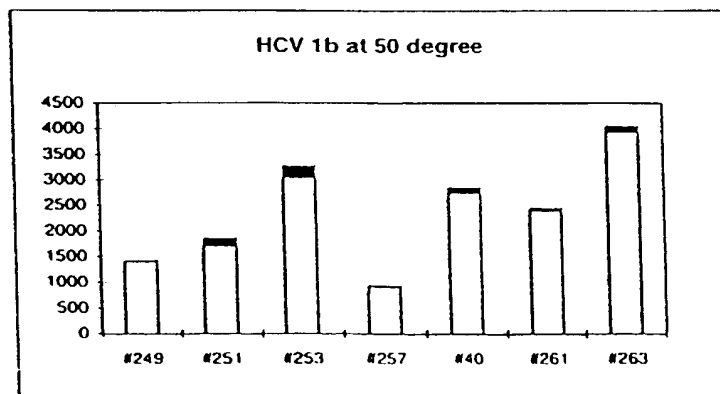
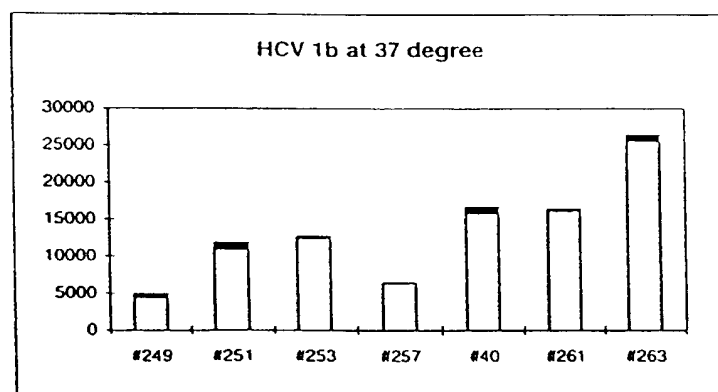
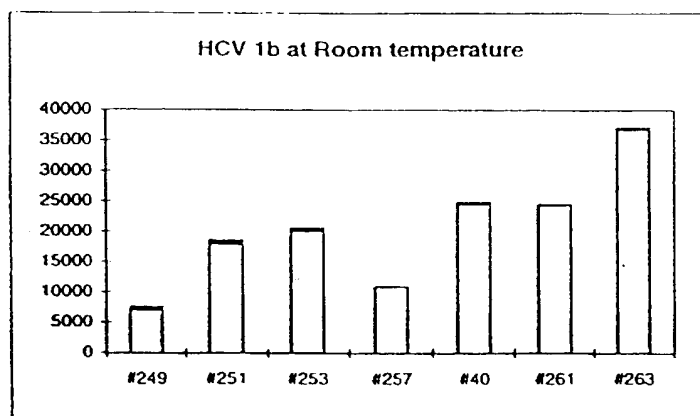


FIGURE 8A



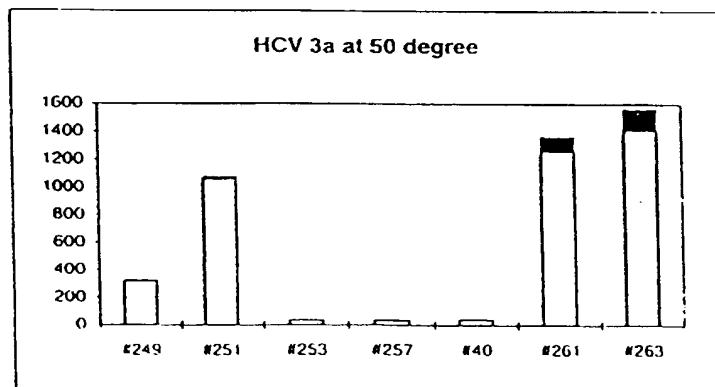
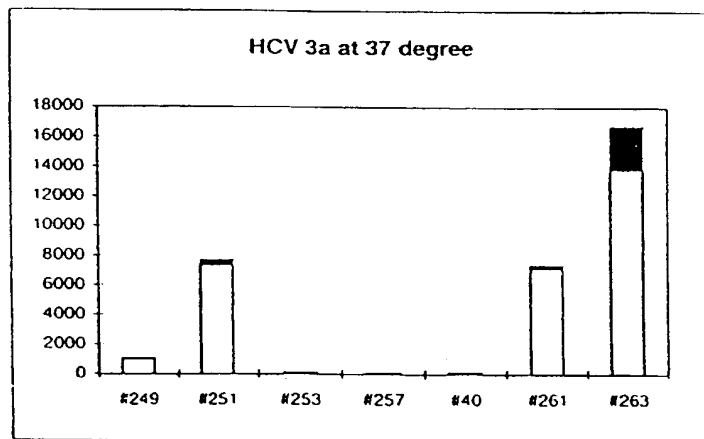
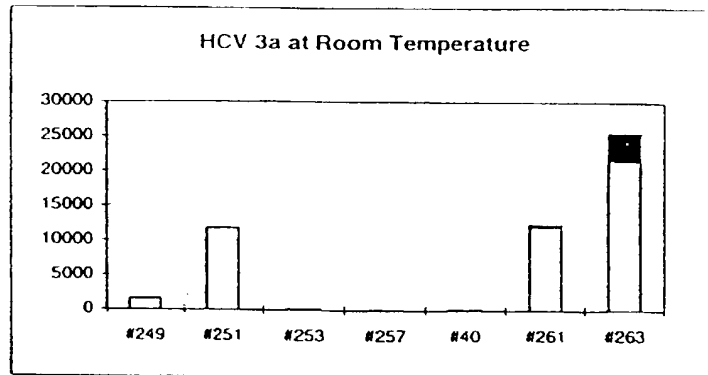
8/123

FIGURE 8B



9/123

FIGURE 8C



10/123

FIGURE 9A

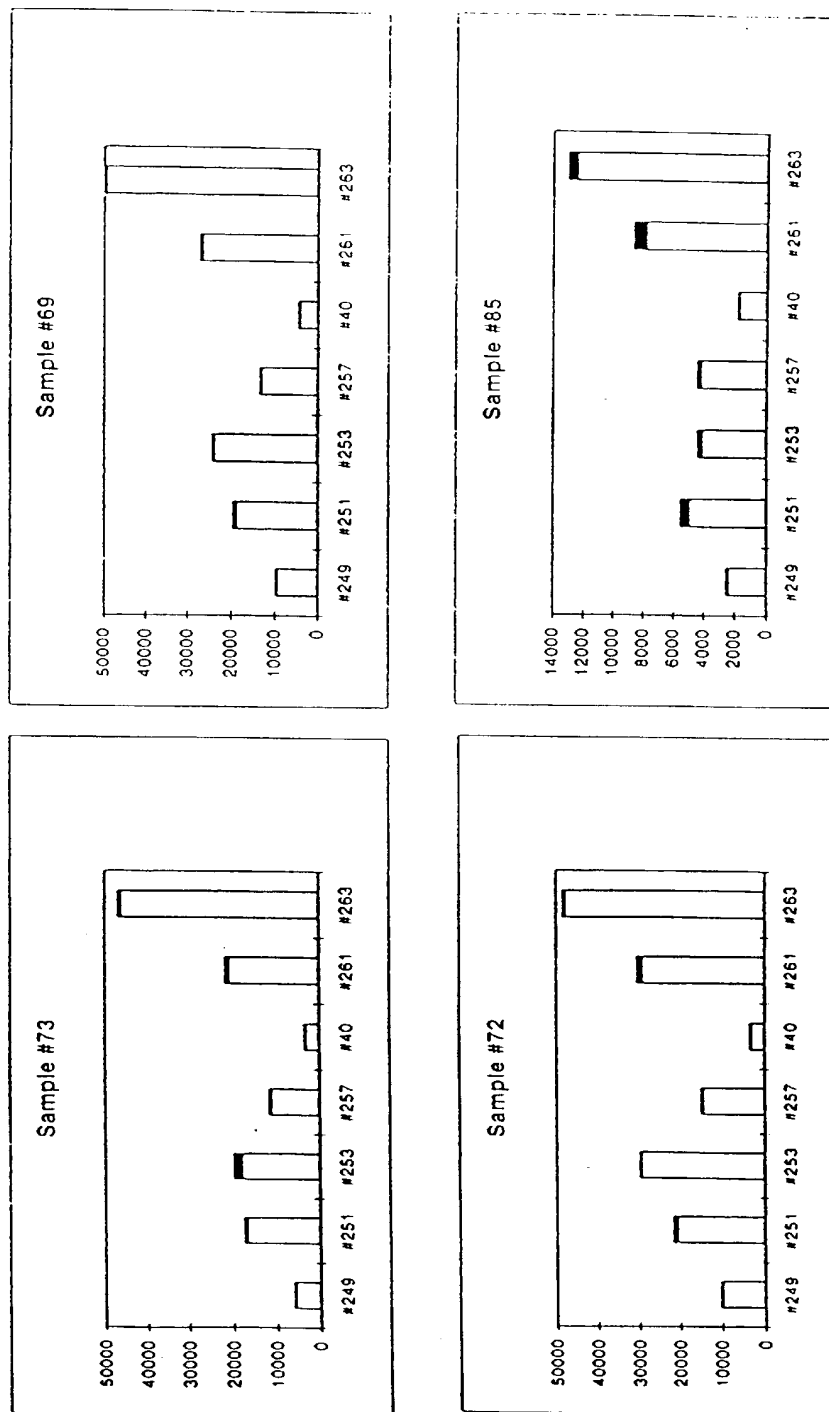


FIGURE 9B

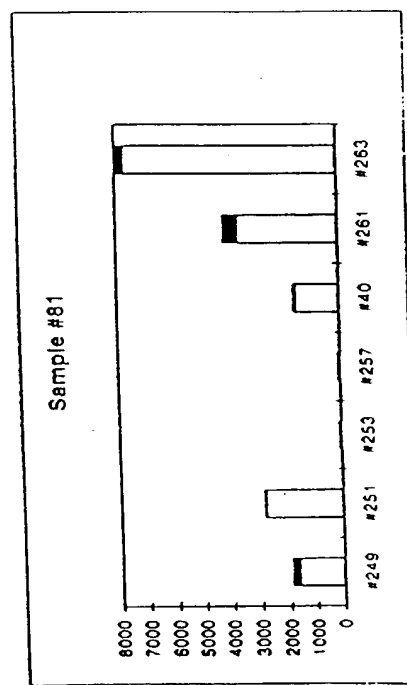
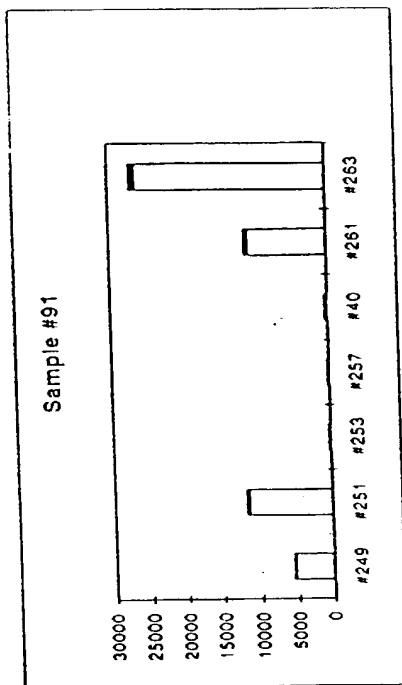
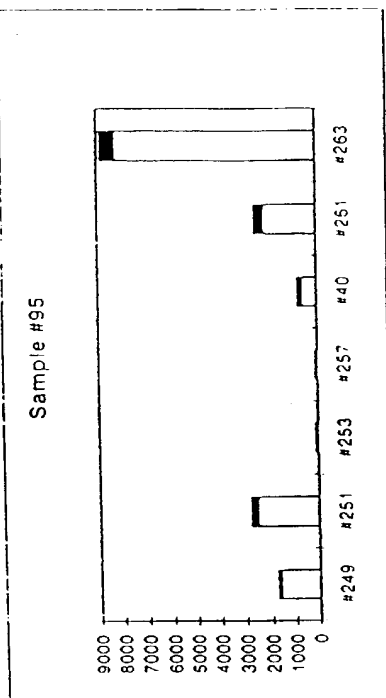


FIGURE 9C

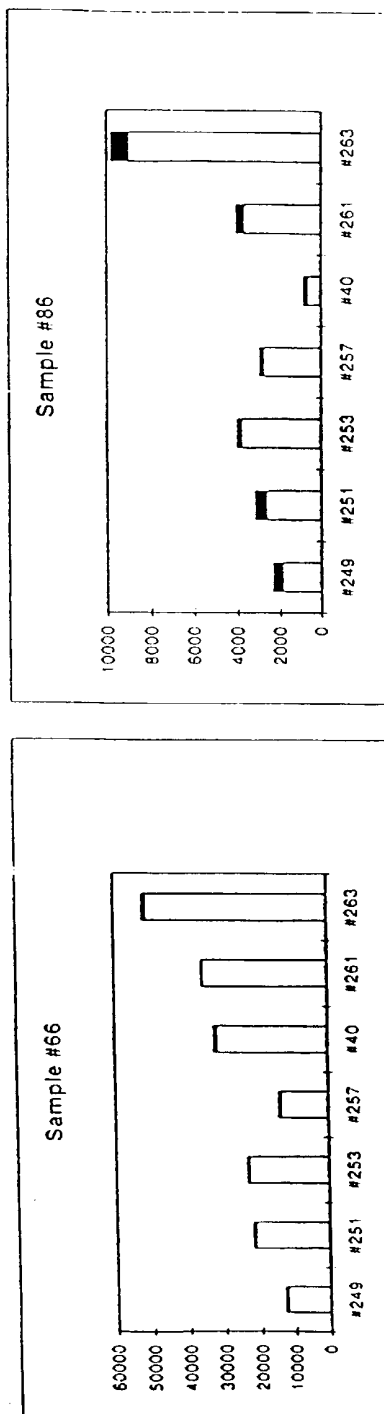
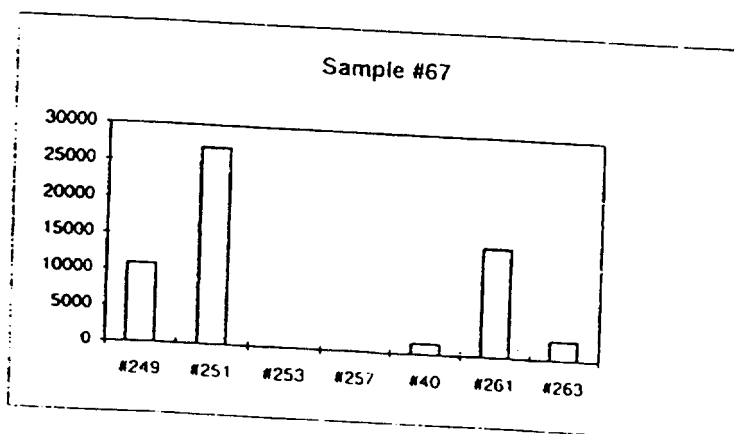
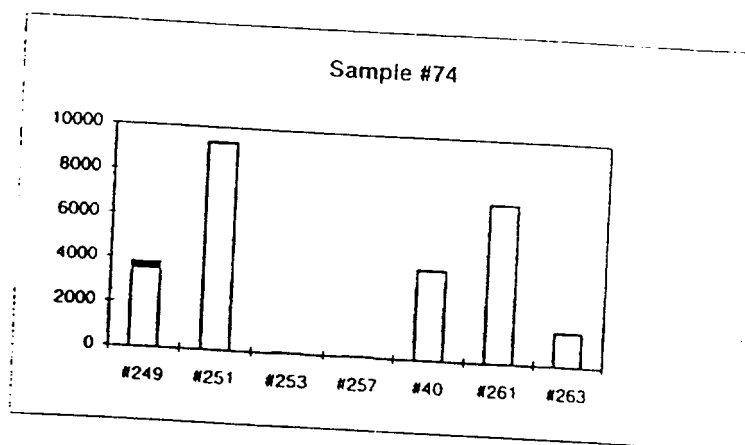


FIGURE 9D



14/123

FIGURE 10

#80

A
G A
T — A
C — G
T — A
G — C
T — A
C — G
G — C
C — G

5'-FlTGCTCTCTGGT TGGTCTCTCGTAAT-3'

#81

A
G A
T — A
C — G
T — A
G — C
T T
C C
G — C
C — G

5'-FlTGCTCTCTGGT TGGTCTCTCGTAAT-3'

#82

G^{AA}
T T
C T
T T
G T
T T
C T
G C
C

5'-FlTGCTCTCTGGT TGGTCTCTCGTAAT-3'

15/
123

0988045 061501
TOST90" sh628860

FIGURE 11A

#2) 5' Biotin

| | | |
|---|---|---|
| | I | |
| | T | A |
| C | G | A |
| A | T | A |
| G | C | G |
| A | T | A |
| C | G | C |
| A | T | A |
| G | C | G |
| C | G | C |
| G | C | G |

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#FD91) 3' Biotin - CGAGAGACCA - 5'

| | | |
|---|---|---|
| | A | |
| G | | A |
| T | A | |
| C | G | |
| T | A | |
| G | C | |
| T | A | |
| C | G | |
| G | C | |
| C | G | |

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'

↓ ↓

#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

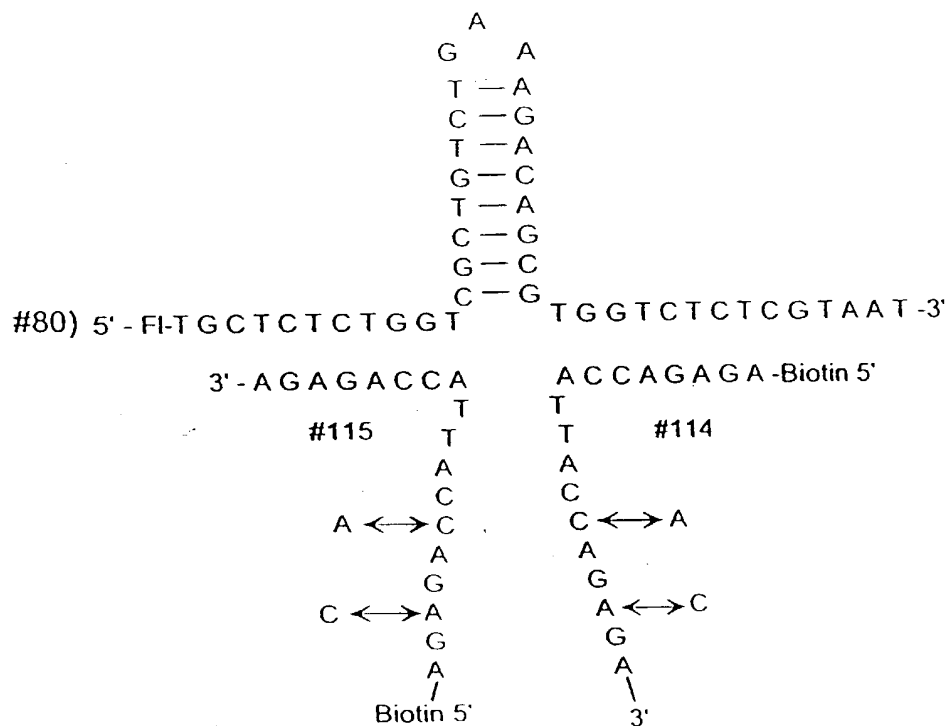
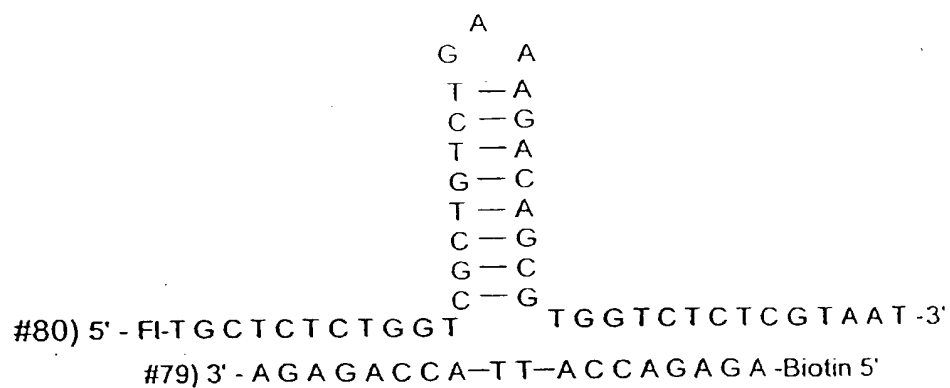
#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT - 5'

16/123

0988945-061501

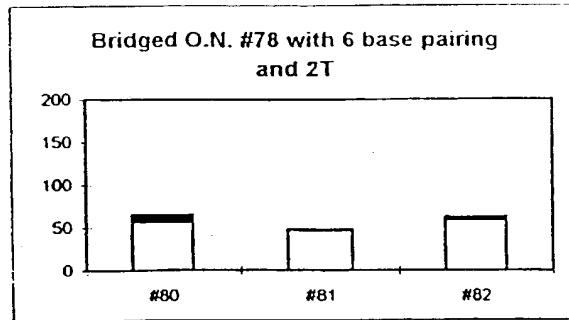
FIGURE 11B



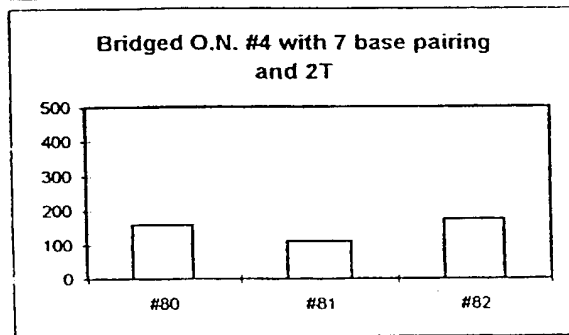
17/123

FIGURE 12

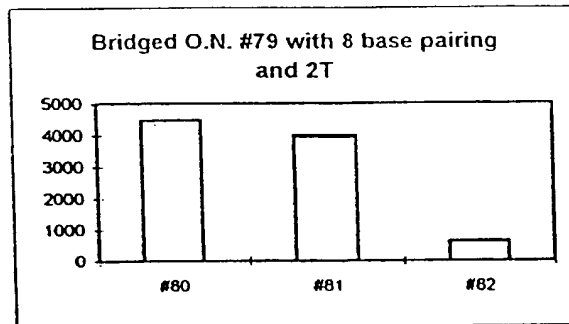
A



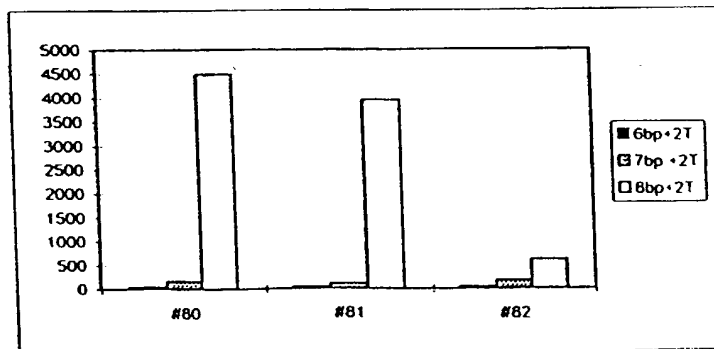
B



C

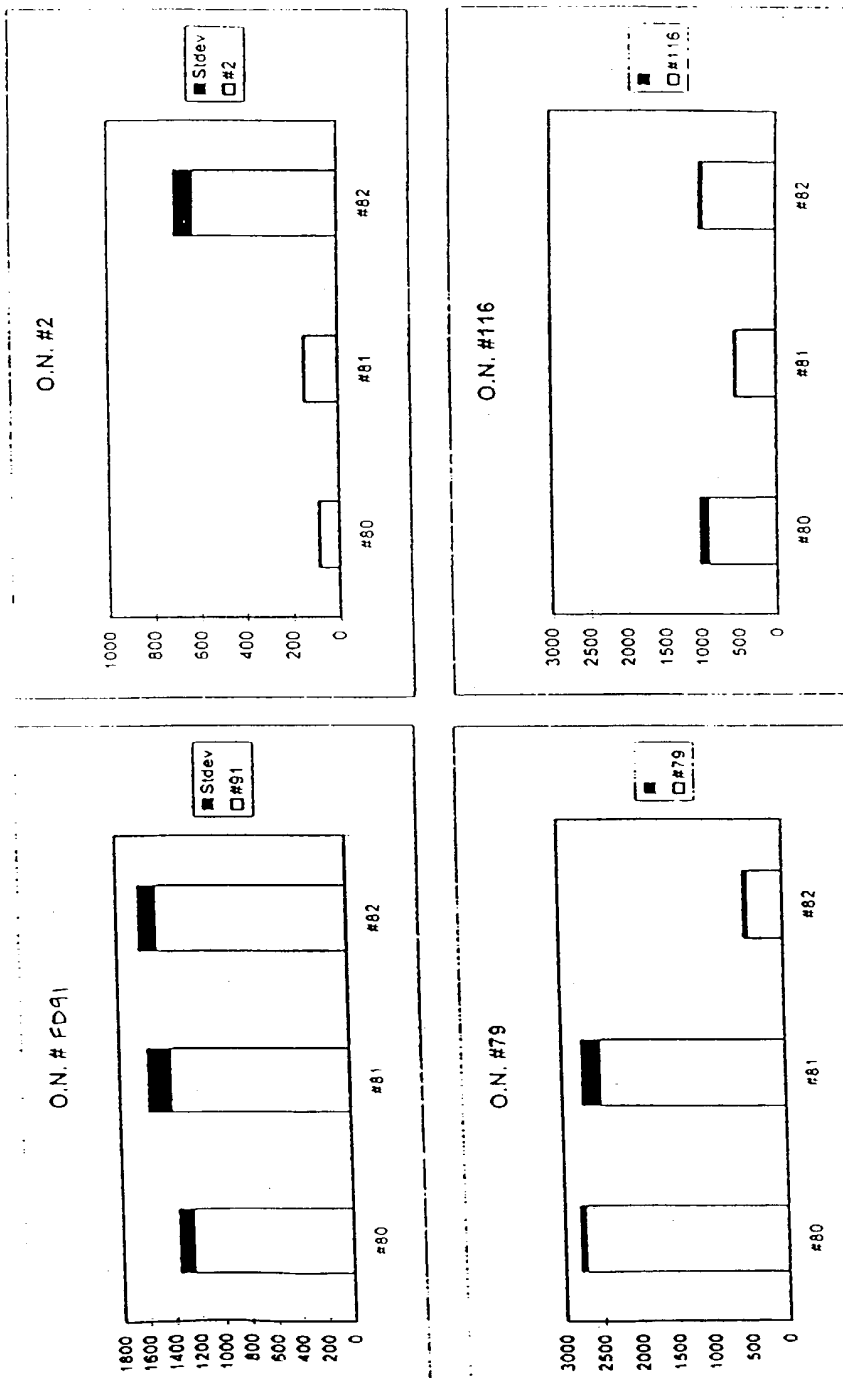


D



18/123

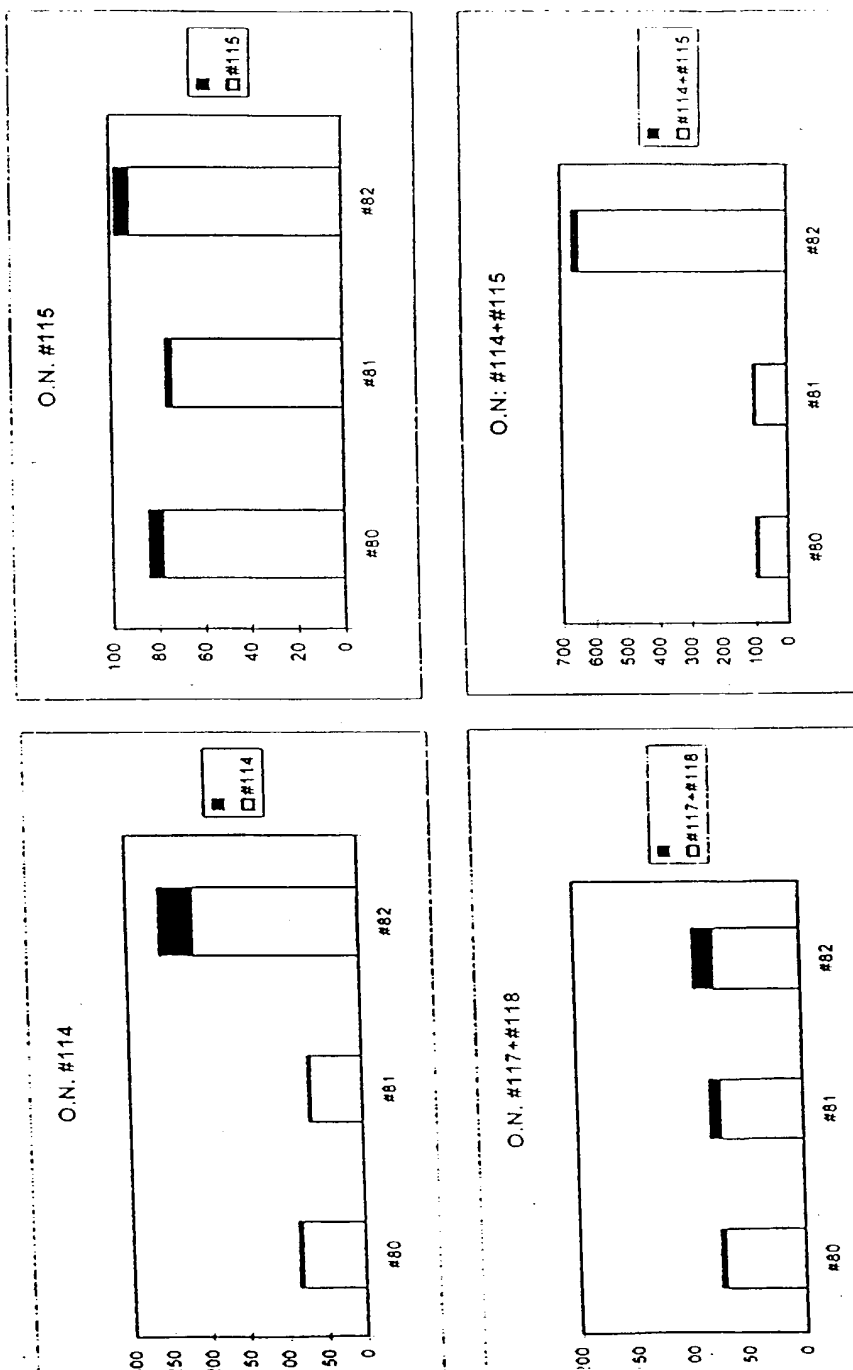
FIGURE 13A



19/123

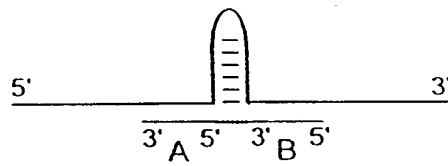
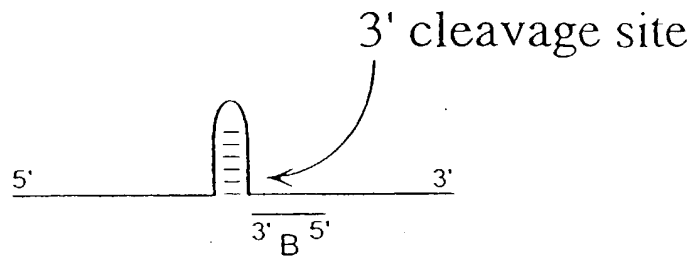
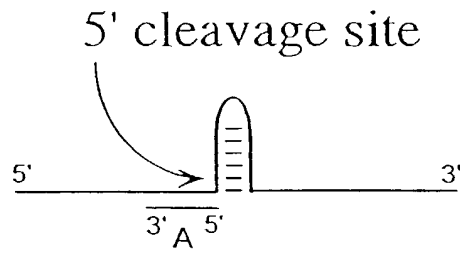
FIGURE 13B

TEST 90" sh623350



20/123

FIGURE 14



| | | | |
|------|--|--|---------|
| | 1 | -----10-----20-----30-----40-----50-----60-----70-----80 | |
| 1a | CTCGAAGCACCCCTATCAGGCAGTACCACAAGG | CCTTCGGCAGCCCAACACTACTGGGCTAGCAGTCTTGC | GGGCACG |
| 1b | | |C |
| 2a/c | | A.....G | |
| 3a | |TGA..c | |
| | -----90-----100-----110-----120-----130-----140-----150-----160 | | |
| 1a | CCCAAATCTCAGGCATTGAGCGGGTTTATCCAAGAAGGACCCGGTGCTCTGGCAATTCCGGGTGTA | CTCACC | GTTTCC |
| 1b | | | |
| 2a/c |GG...A...T |A...T..c | |
| 3a |T.hg.T...l.....GT |AC..CA..hg | |
| | -----170-----180-----190-----200-----210-----220-----230-----240 | | |
| 1a | cCAGACCACCTATG | CTCTCCCCGAGGGGGGTCTCTGGAGGCTGCACGACACTCATATACTAACGCCATGGCTAGACGCTTTC | |
| 1b |ll | | |
| a/c |l |G.....T | |
| 3a |l |G | |

FIGURE 16A

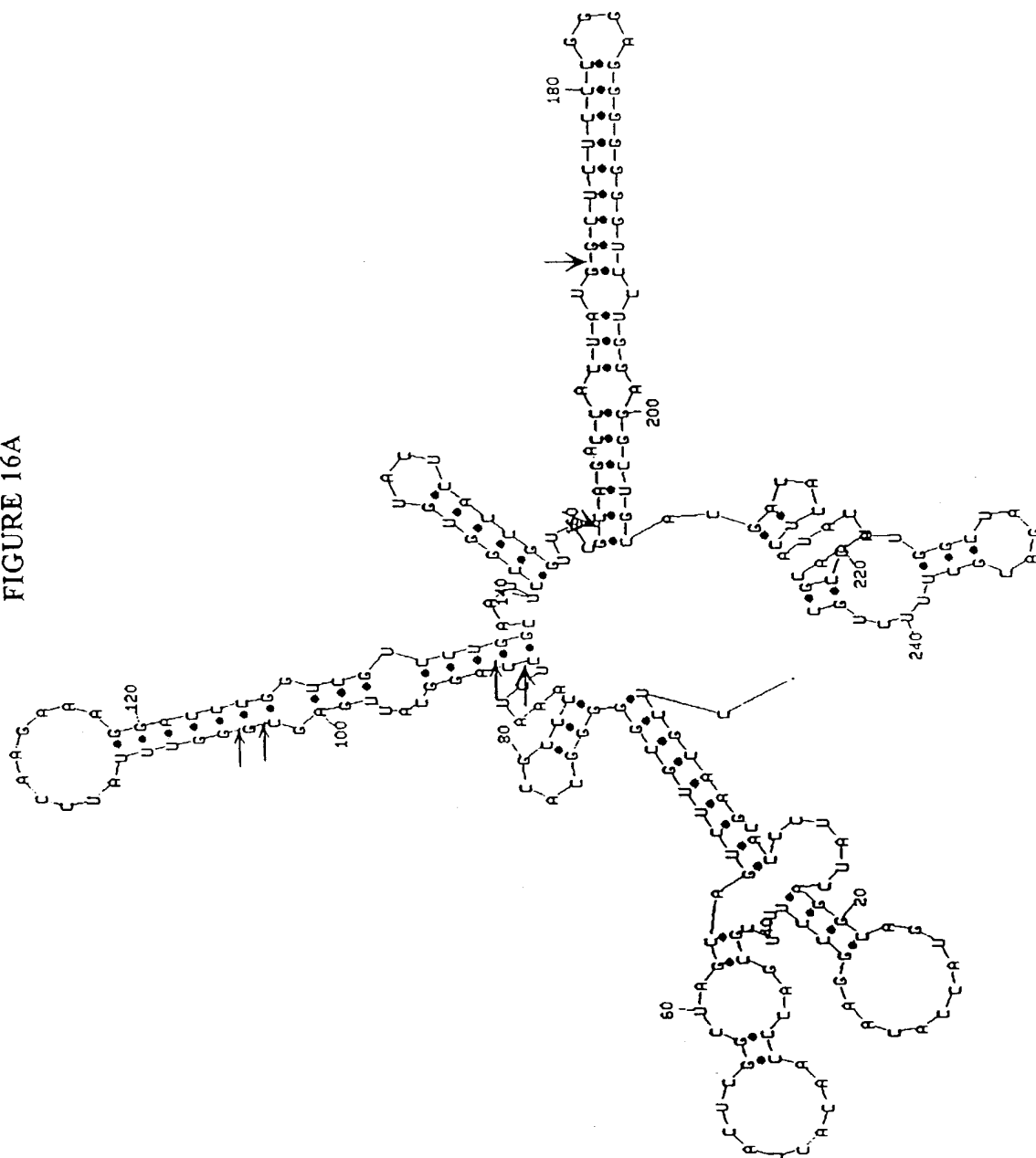
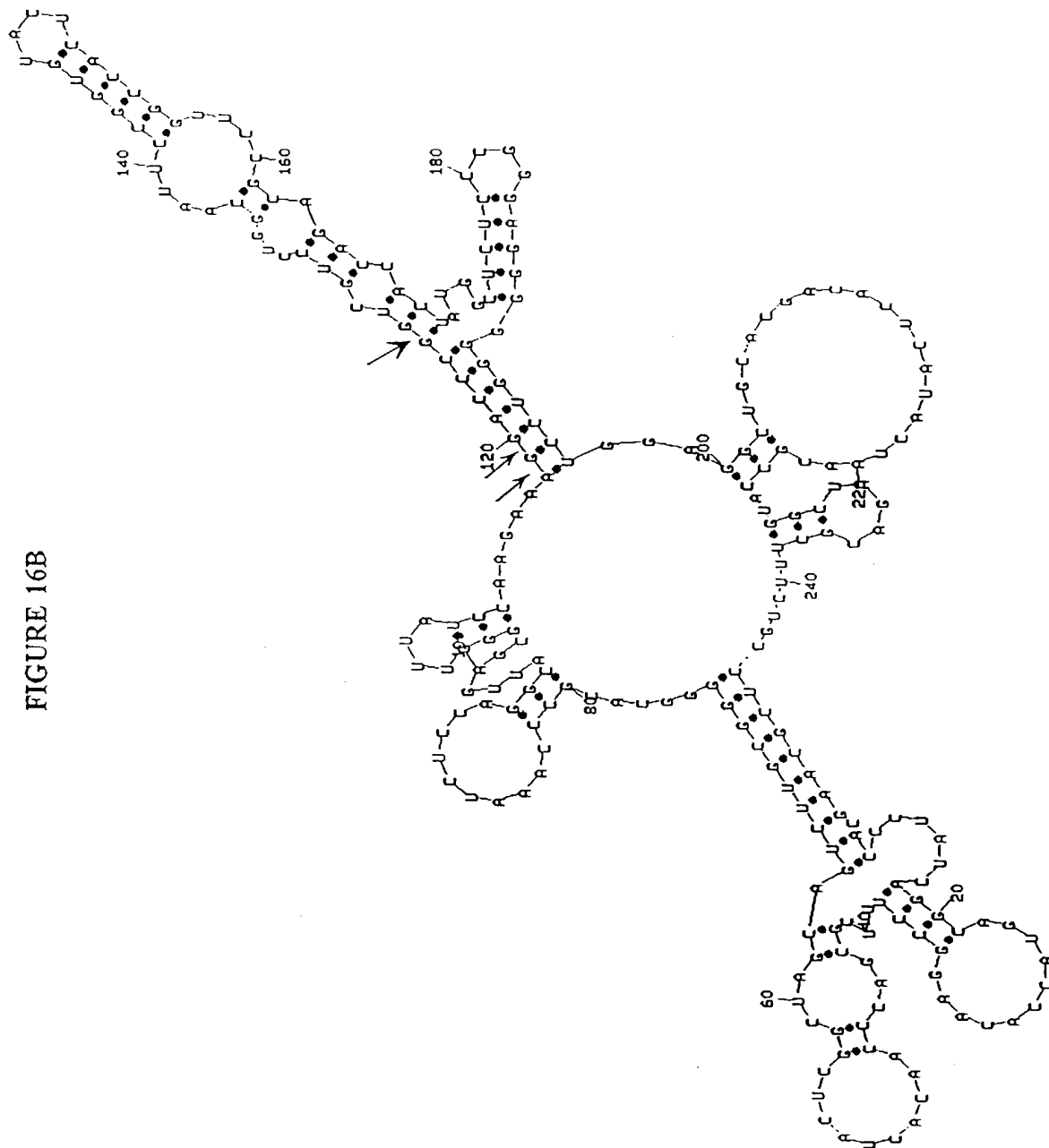
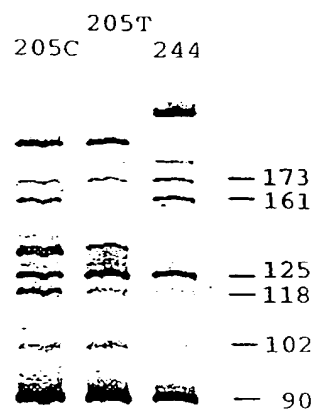


FIGURE 16B



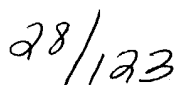
0988345 01501
TOSTAD 54628860

FIGURE 17A



25/123

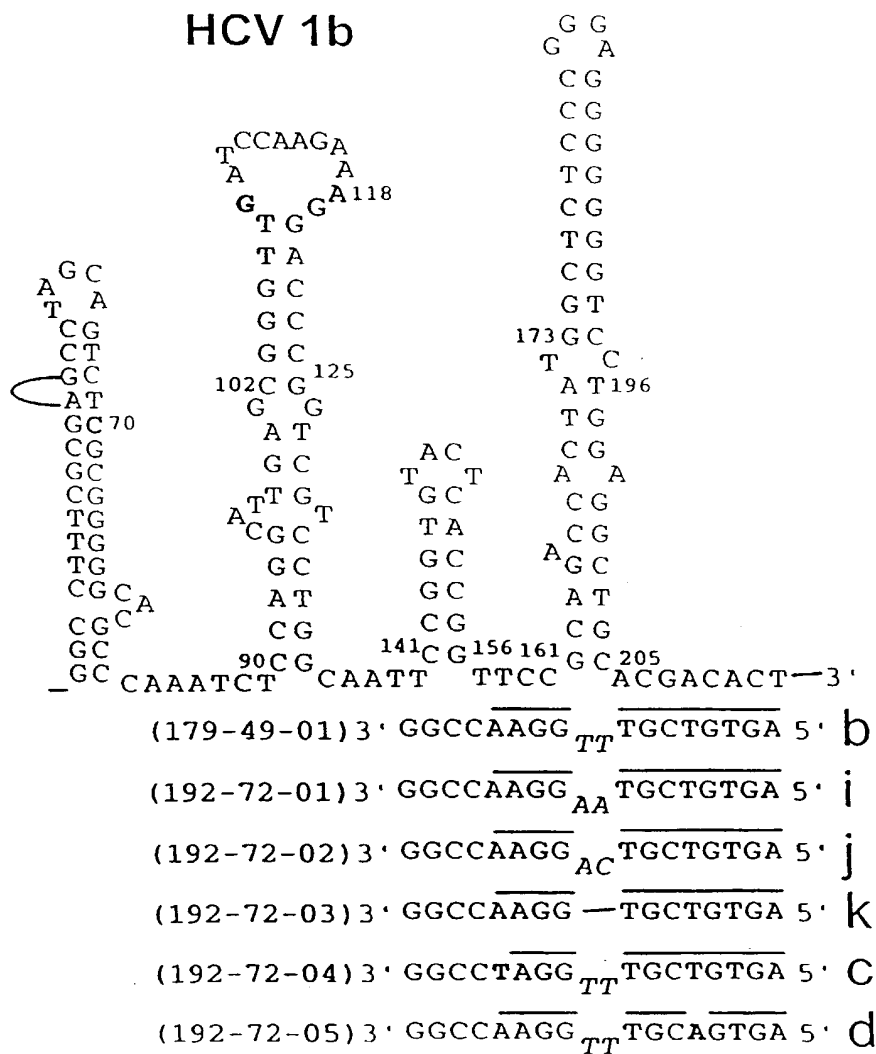
Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector x for a specific value of n . The x-axis for all histograms is labeled 'x' and ranges from 0 to 120. The y-axis is labeled 'count'. The histograms are for $n = 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120$. As n increases, the distribution of non-zero elements shifts to the right, indicating that more elements in the vector x are non-zero for larger n . The peak count also increases significantly with n .

[illegible]

28/123

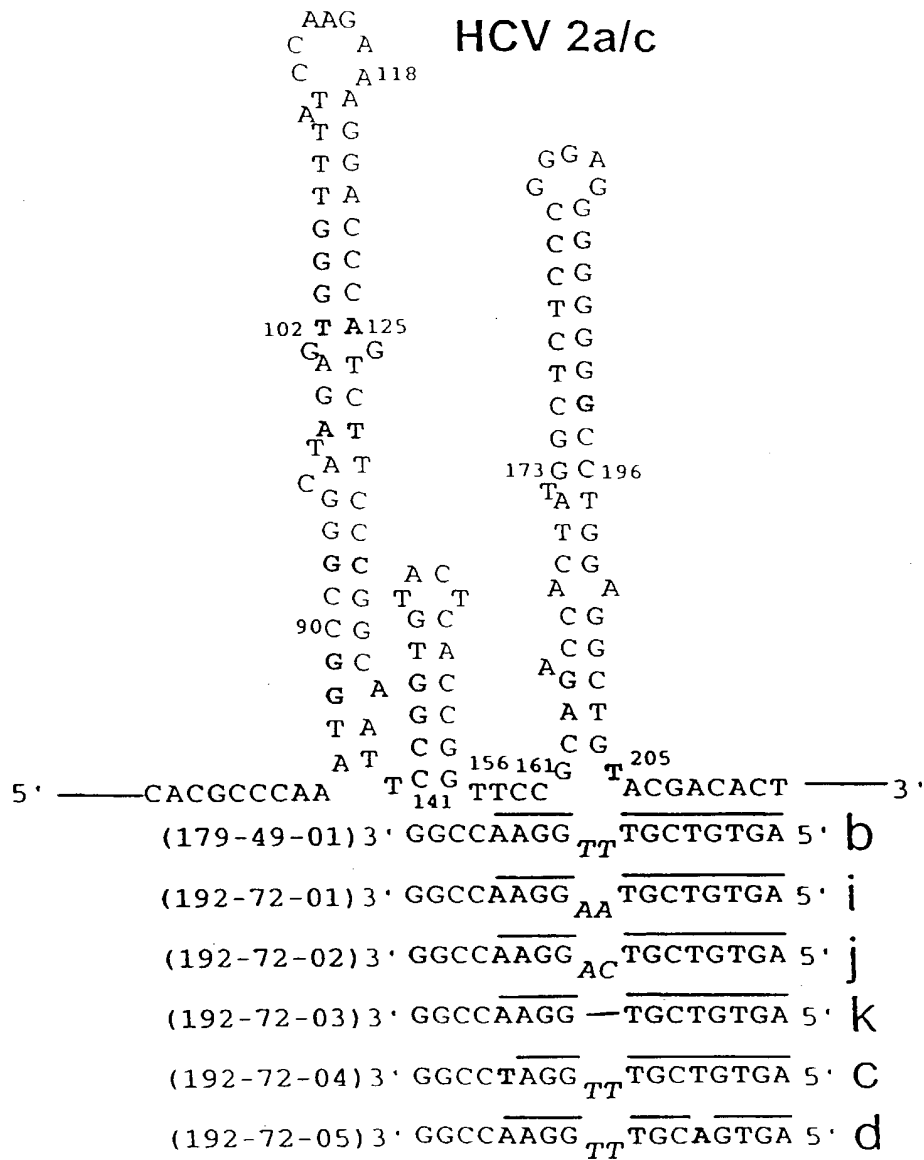
FIGURE 18B

HCV 1b



29/123

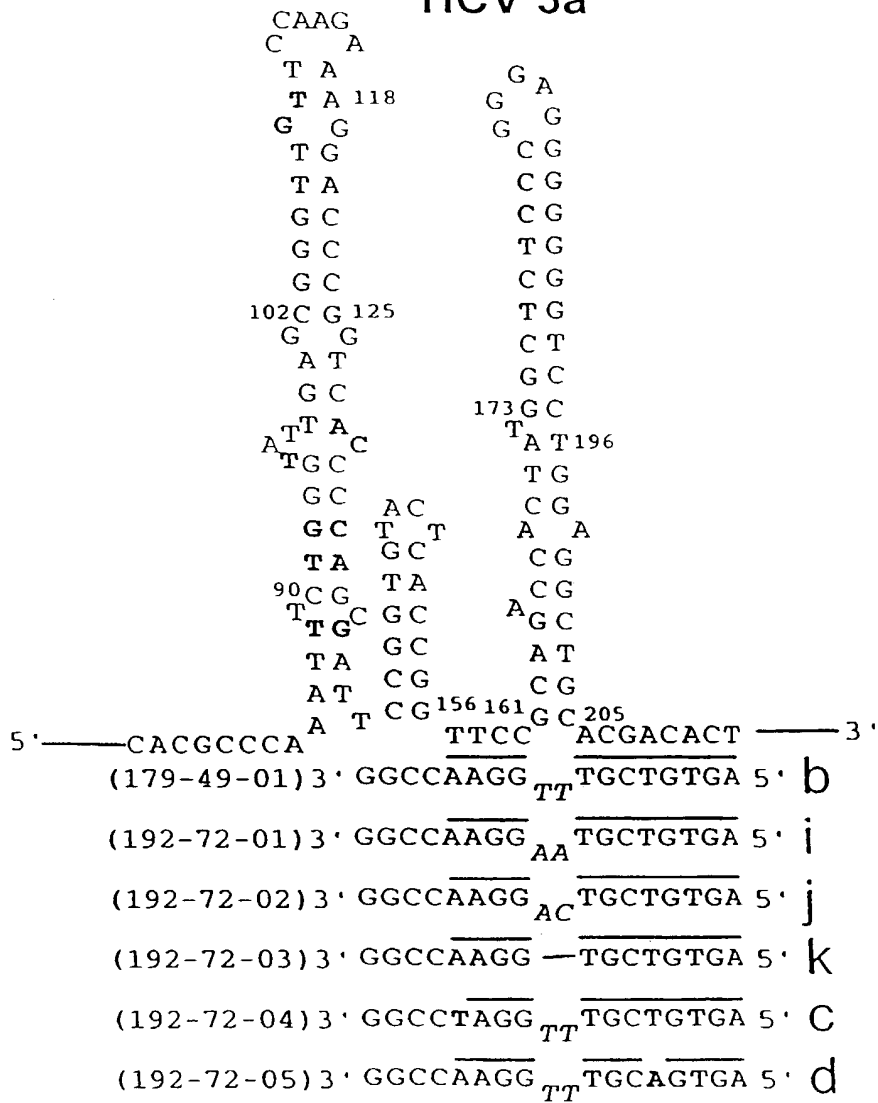
FIGURE 18C



30/123

FIGURE 18D

HCV 3a



31/123

FIGURE 19

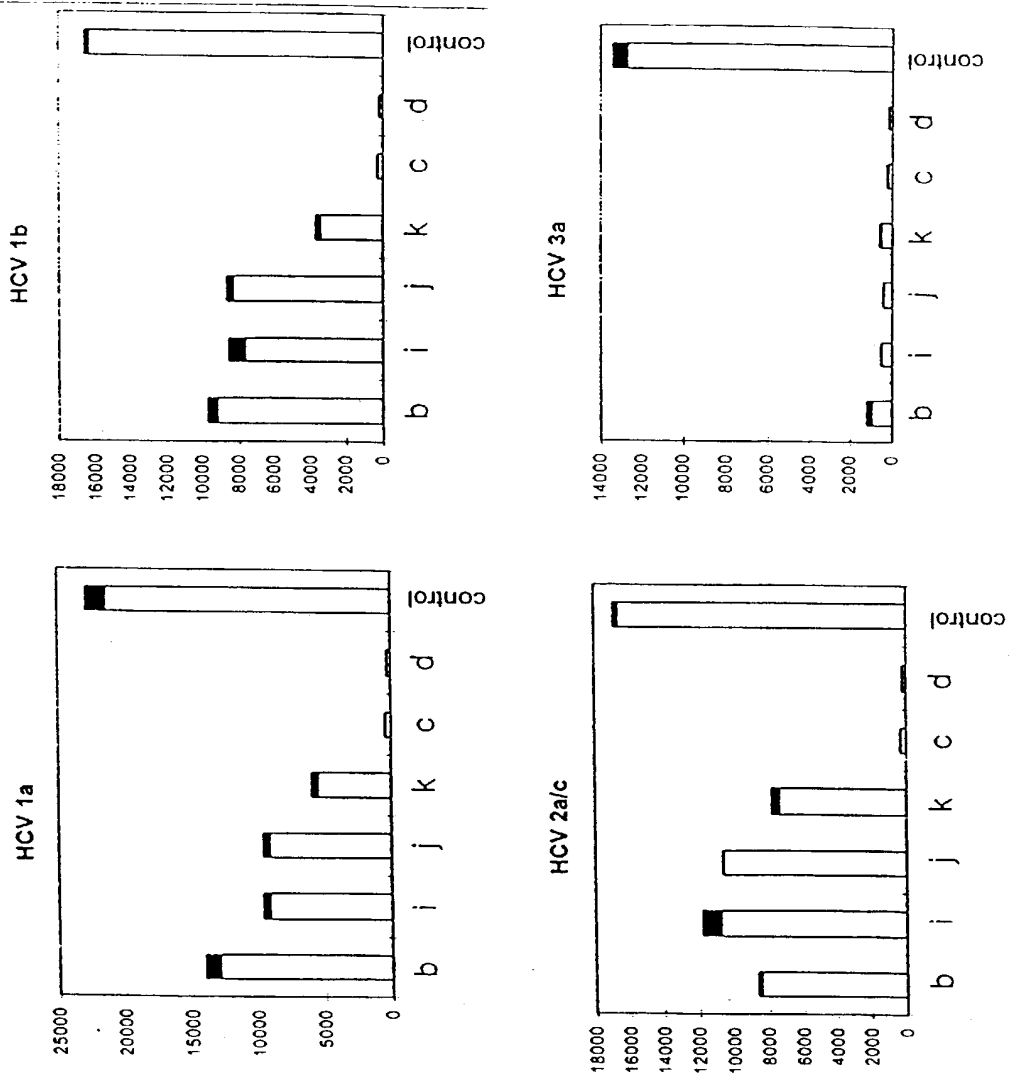
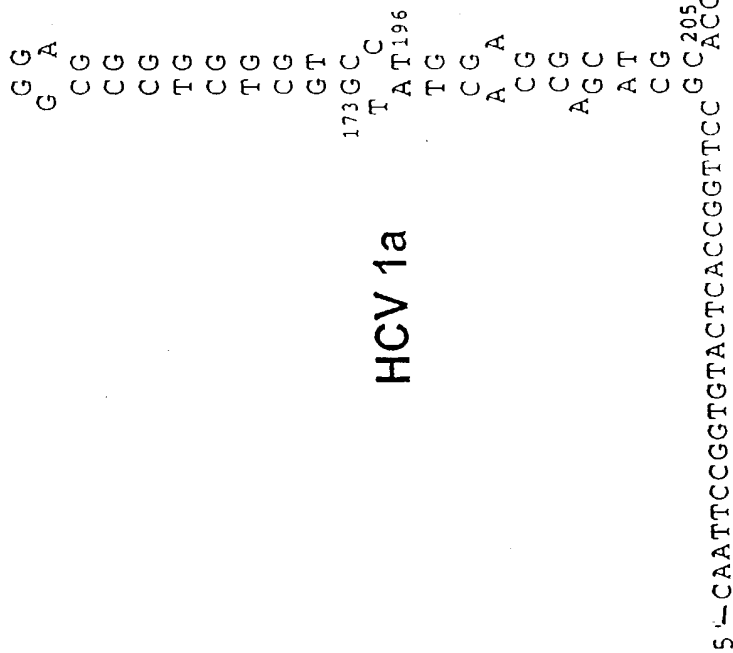
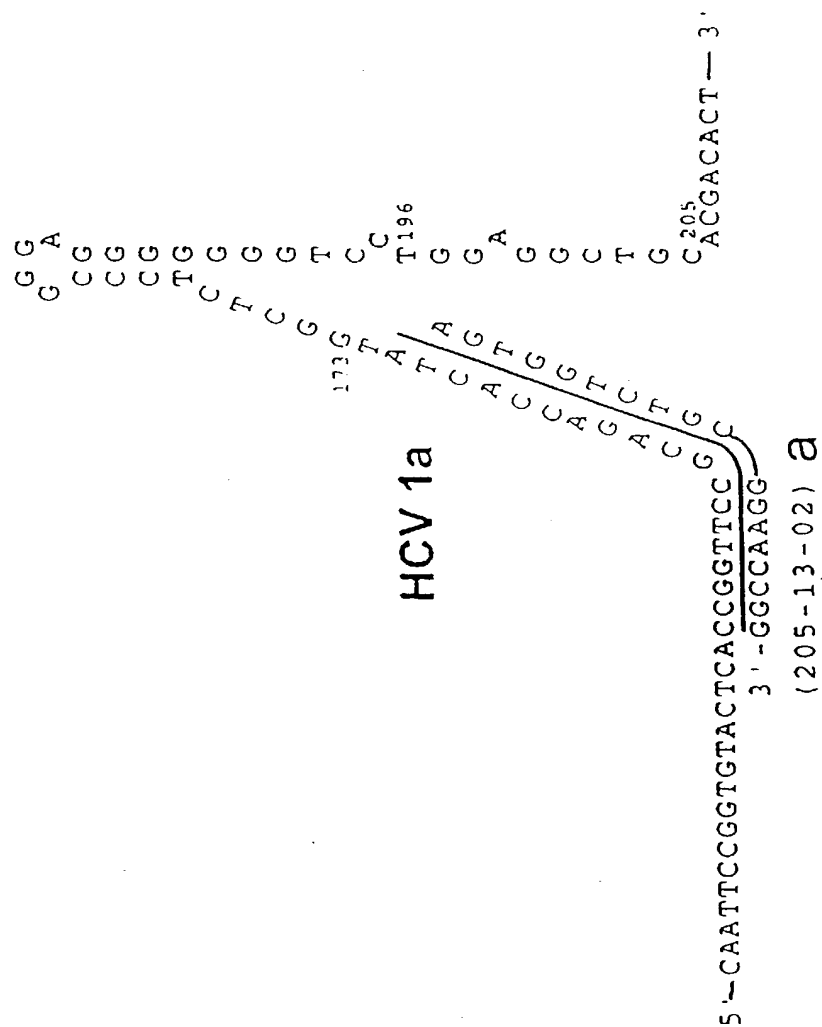


FIGURE 20A



- a 3'-GGCCAAAGGCGTCTGGTGA-F1'5' (205-13-02)
- b 3'-GGCCAAAGG_{TT}TGCTGTGA-F1'5' (179-49-01)
- c 3'-GGCCTAGG_{TT}TGCTGTGA-F1'5' (192-72-04)
- d 3'-GGCCAAAGG_{TT}TGCAGTGA F1'5' (192-72-05)
- e 3'-GGCCAAAGG-F15' (205-27-01)

FIGURE 20B



170

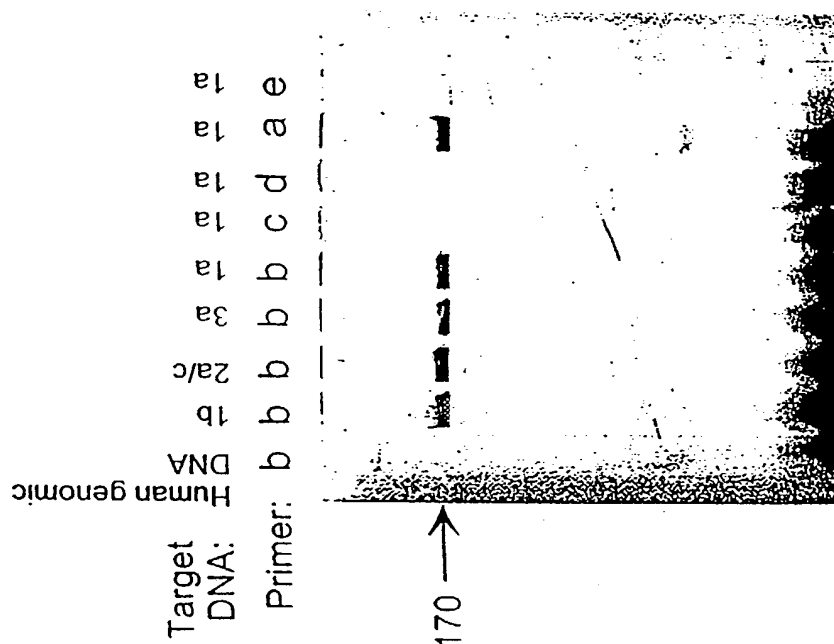
$$35/123$$


FIGURE 22

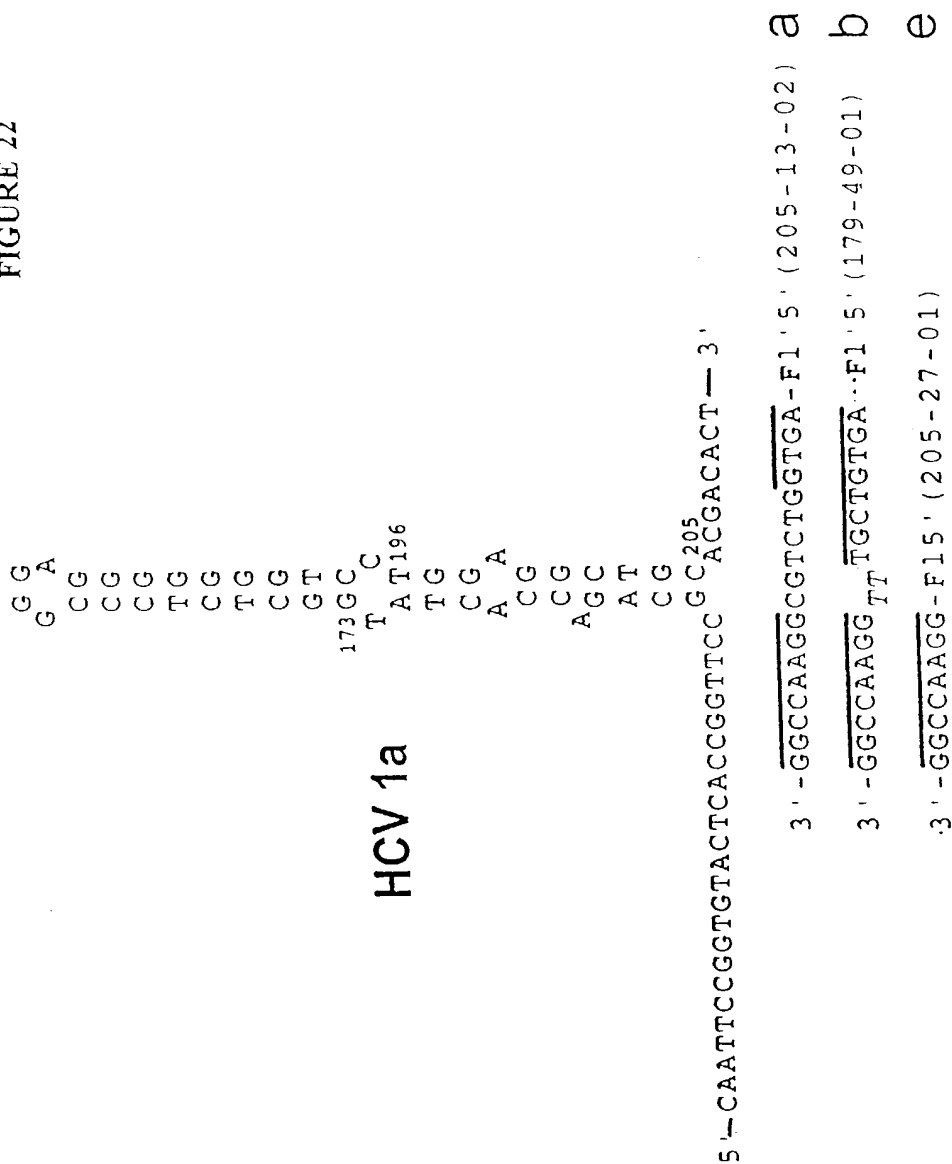
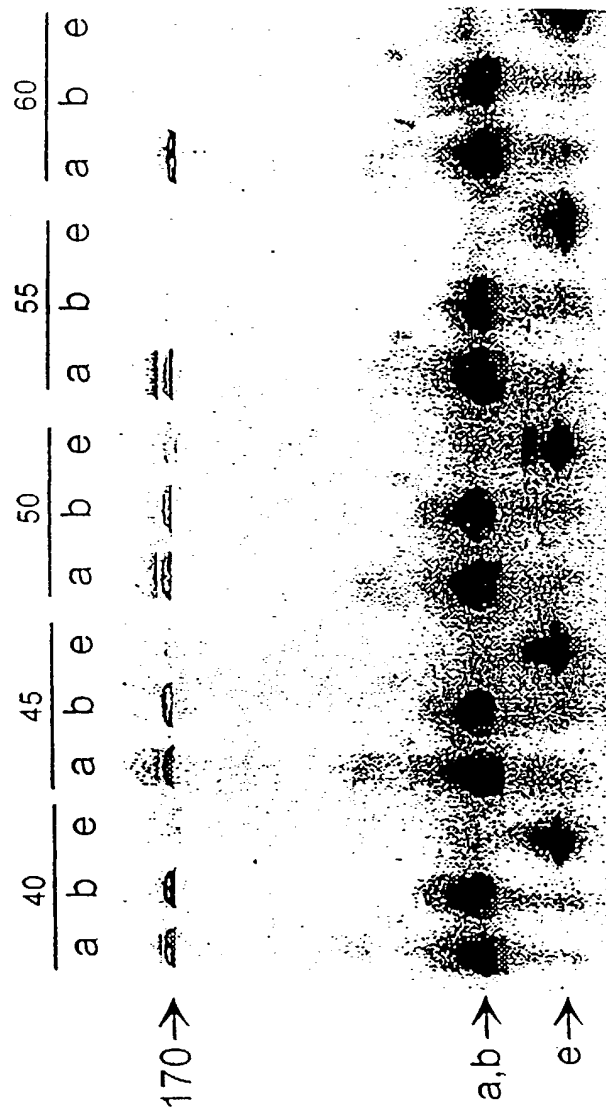


FIGURE 23



37/123

FIGURE 24

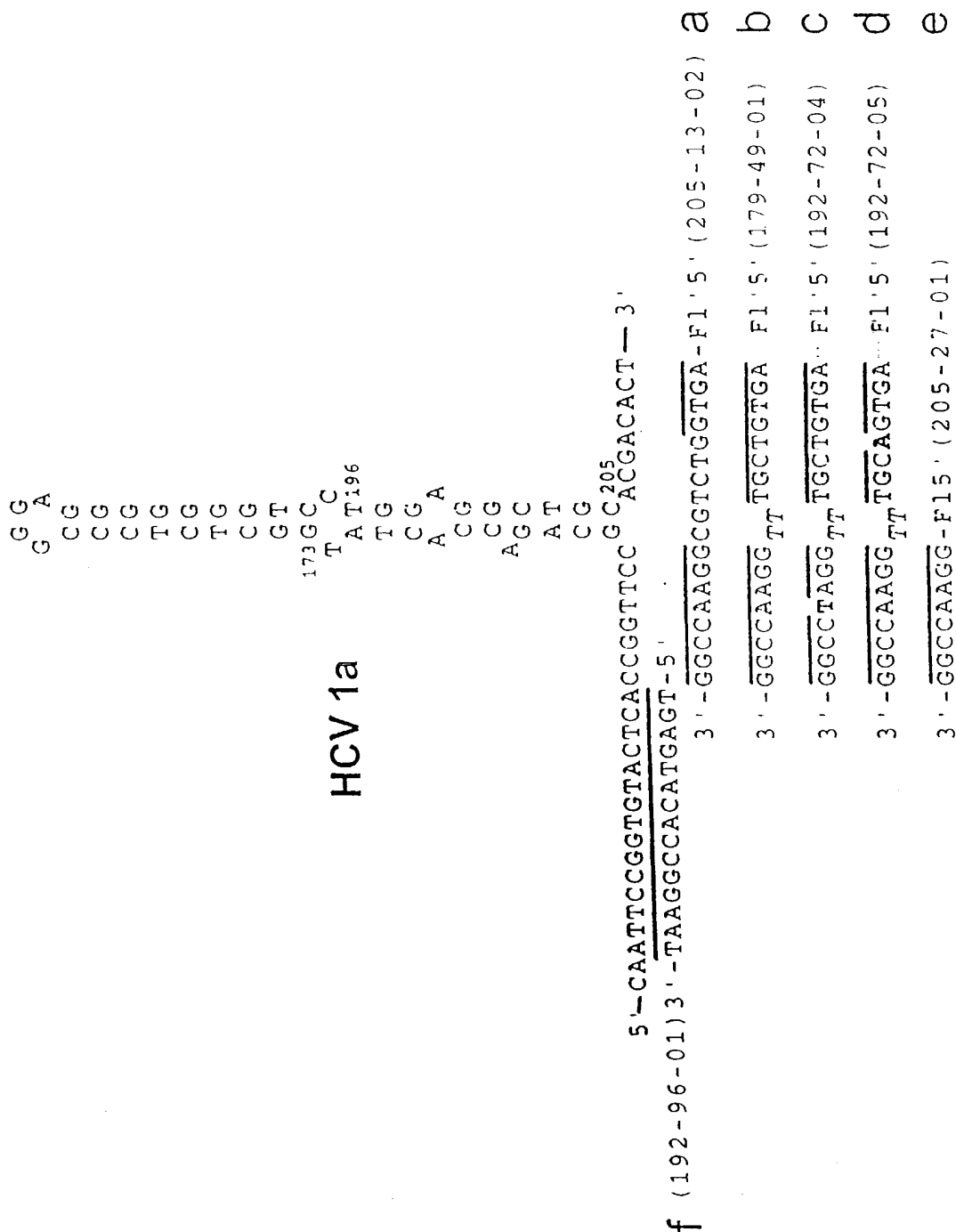


FIGURE 25

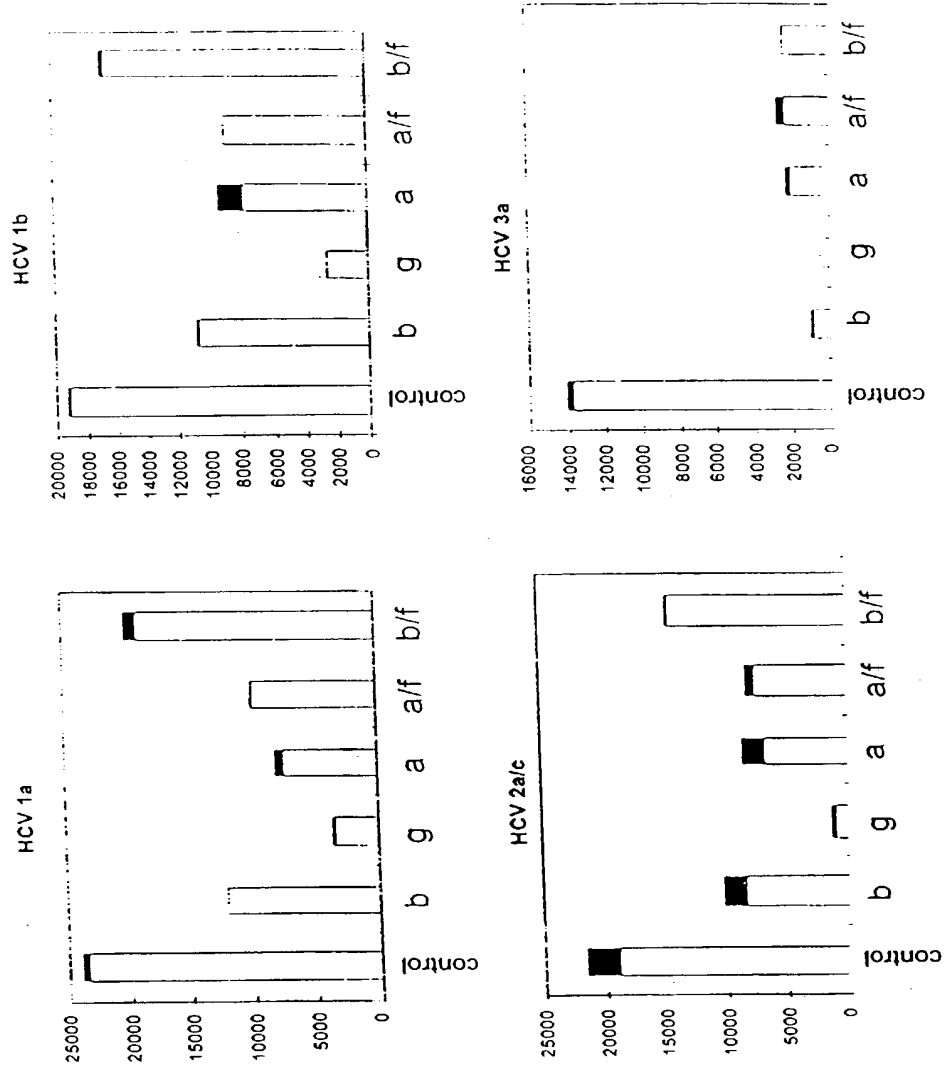


FIGURE 26

5'-ATTCCGGTGTACTCACCGGTTCCAAACGACACT-3' (205-13-01) S.T.
f (192-96-01) 3'-TAAGGCCACATGAGT-5'
3'-GGCCAAAGCGTCTGGTGA-F1'5' (205-13-02) a
3'-GGCCAAAGG_{TT}TGCTGTGA---F1'5' (179-49-01) b
3'-GGCCTAGG_{TT}TGCTGTGA---F1'5' (192-72-04) c
3'-GGCCAAAGG_{TT}TGCAGTGA F1'5' (192-72-05) d
3'-GGCCAAAGG-F15' (205-27-01) e

FOST 90" 54628860

FIGURE 28



42/123

FIGURE 29A

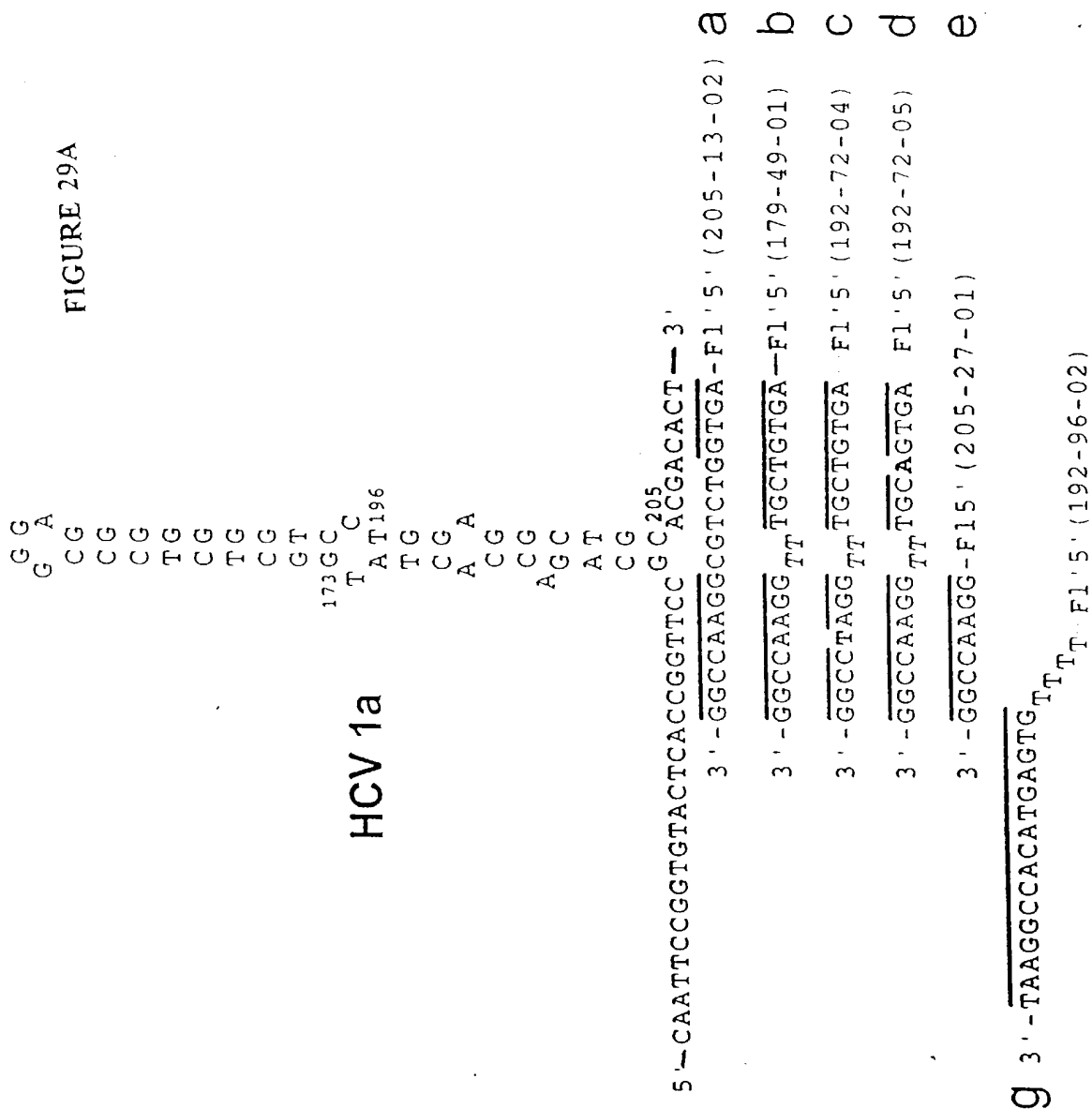


FIGURE 29B

5' -ATTCCGGTGTACTCACC GGTTCCAAACGACACT-3' (205-13-01) S.T.
 3' -GGCCAAAGCGCTCTGGTGA-F1'5' (205-13-02) a
 3' -GGCCCAAGG_{TT} TGCTGTGA--F1'5' (179-49-01) b
 3' -GGCCCTAGG_{TT} TGCTGTGA--F1'5' (192-72-04) c
 3' -GGCCCAAGG_{TT} TGCAGTGA--F1'5' (192-72-05) d
 3' -GGCCCAAGG-F15' (205-27-01) e
 g 3' -TAAGGCCACATGAGTG_{TT} T_T--F1'5' (192-96-02)

[illegible]

FIGURE 30

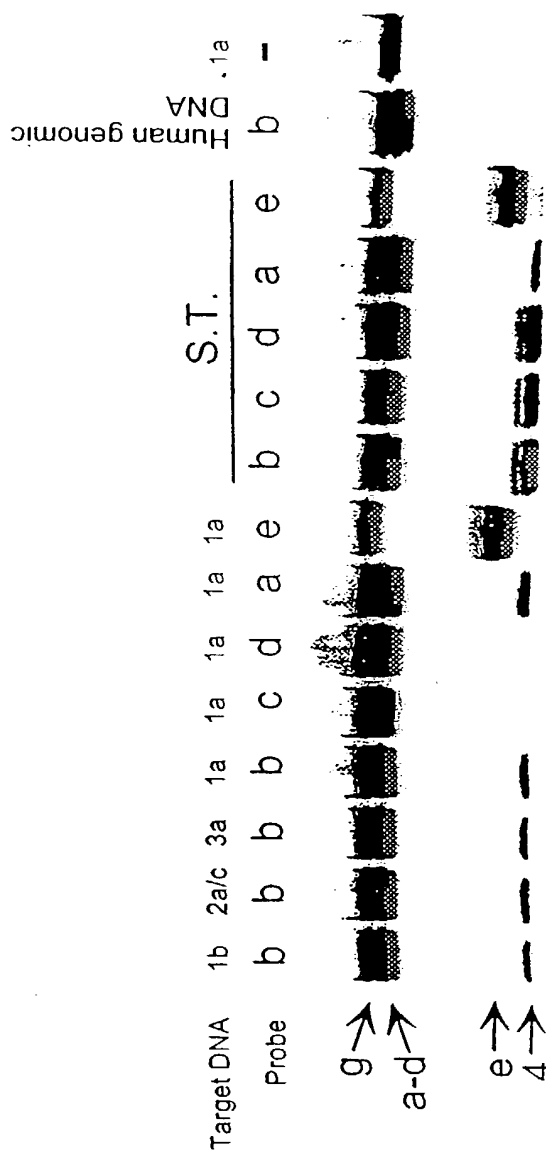

$$45/123$$

FIGURE 31

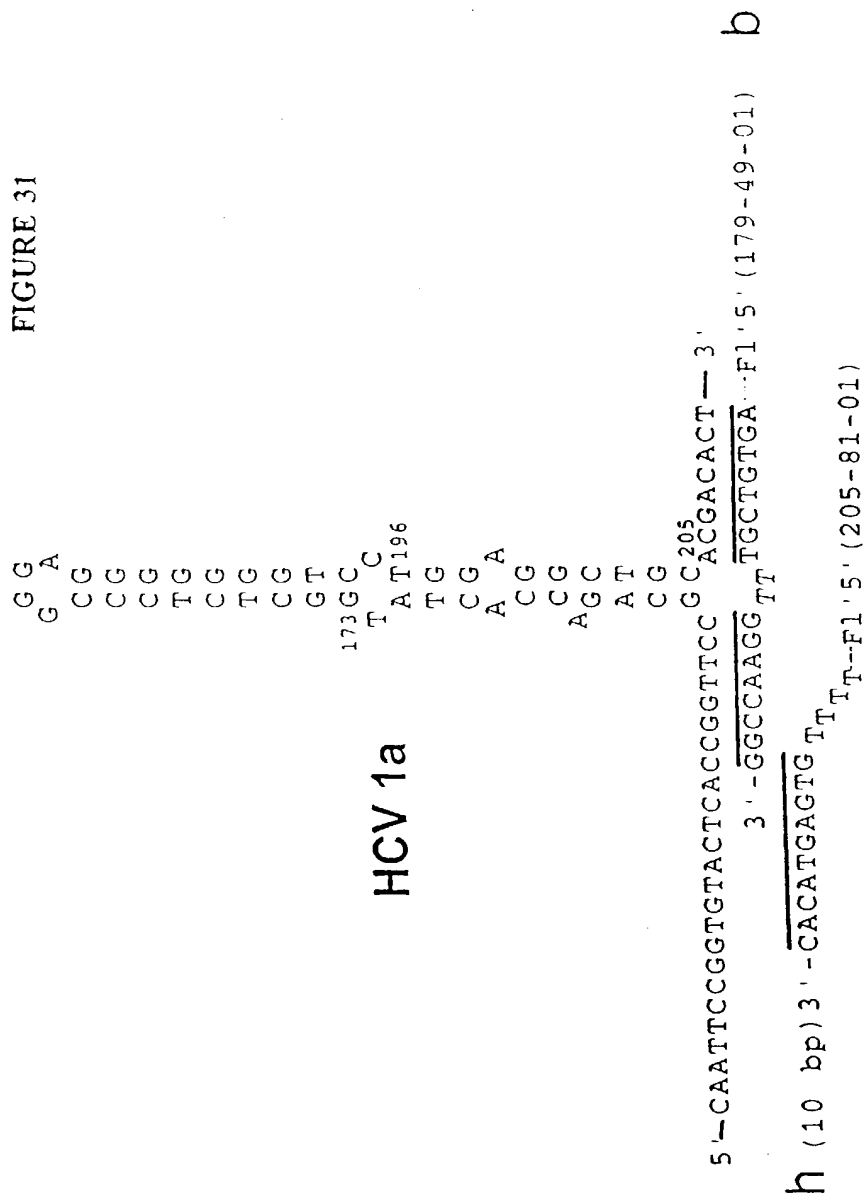
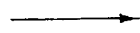


FIGURE 34

STEPS

a



b



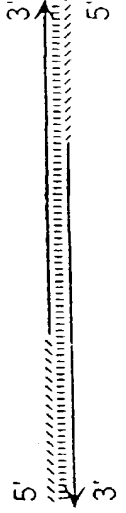
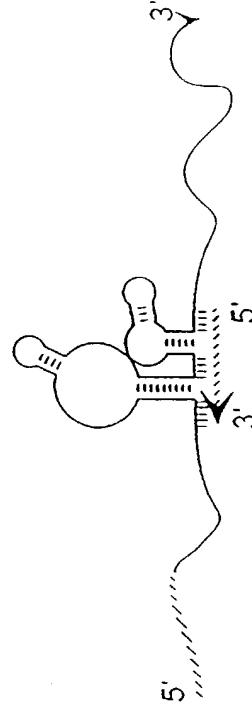
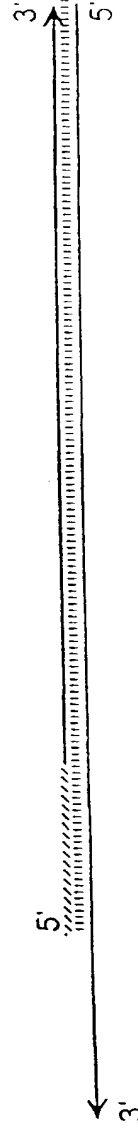
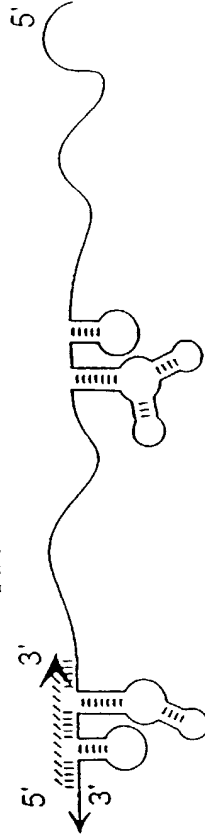
c



d

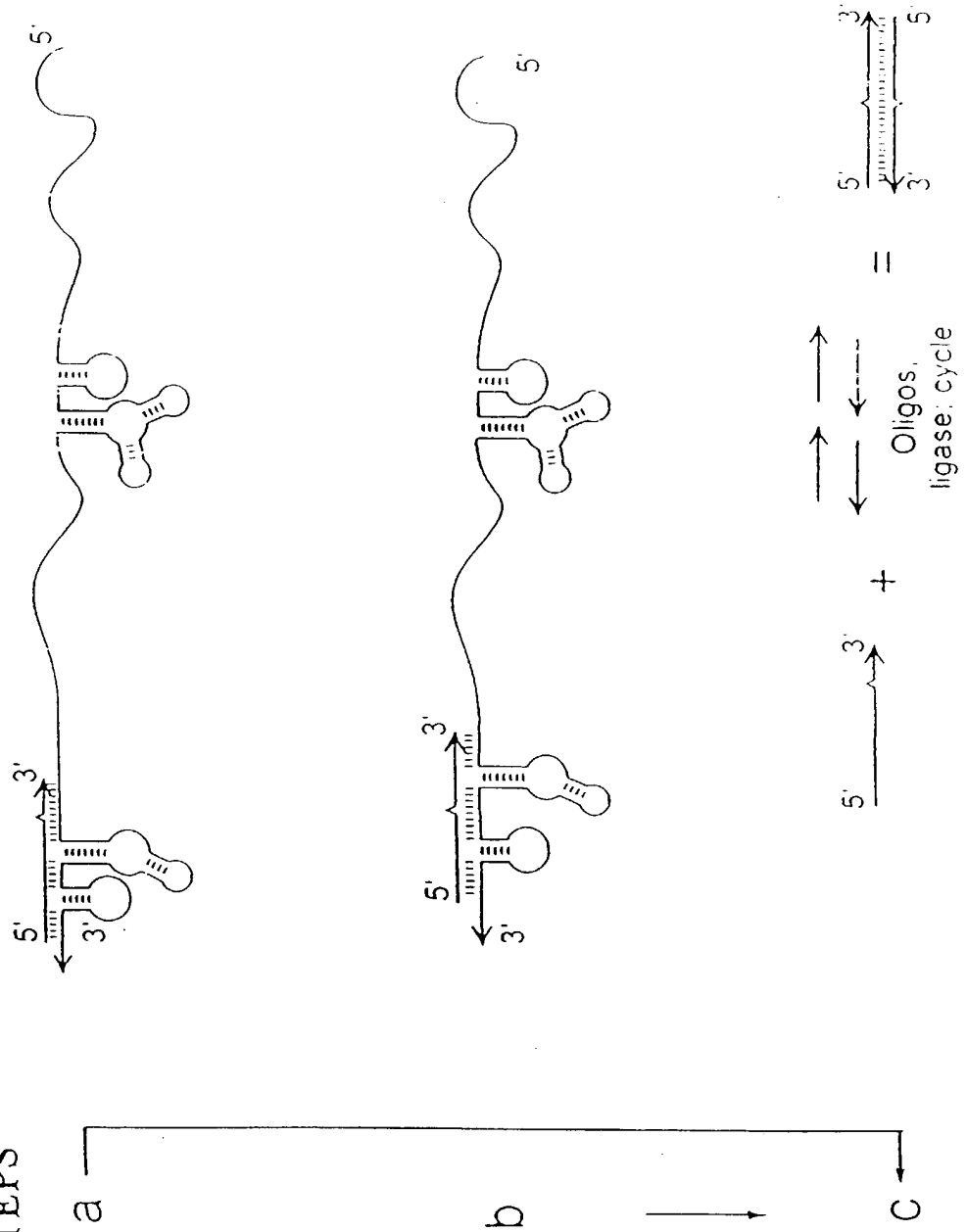


e



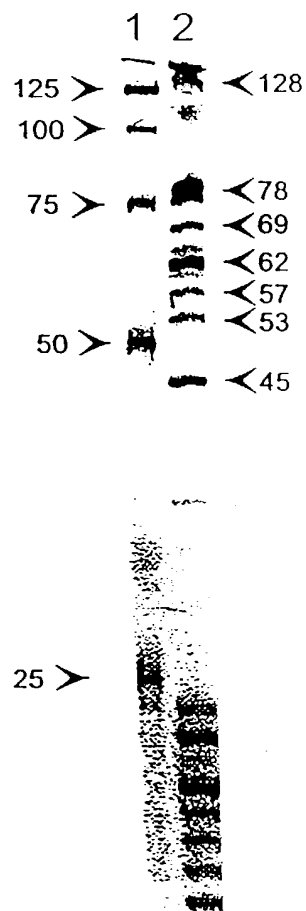
STEPS

FIGURE 35



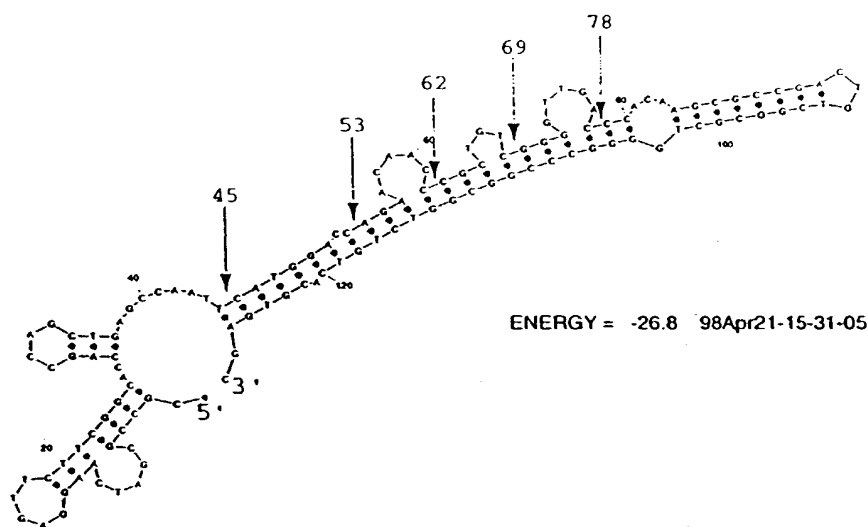
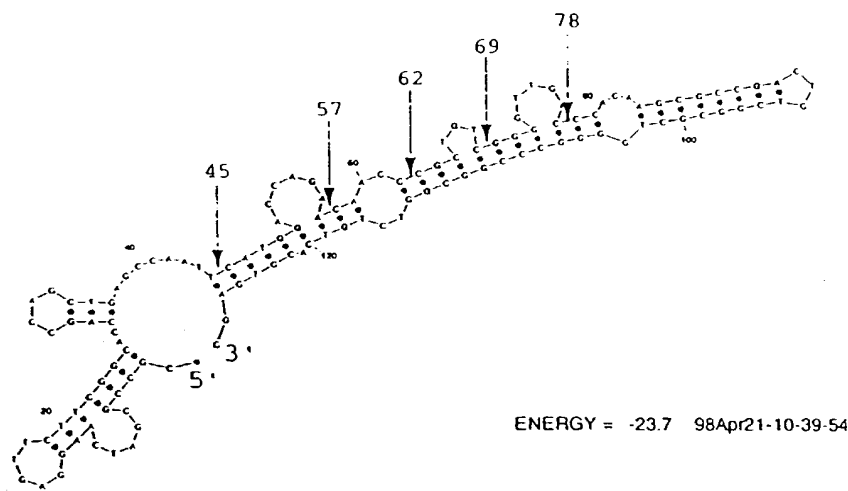
50/123

FIGURE 36



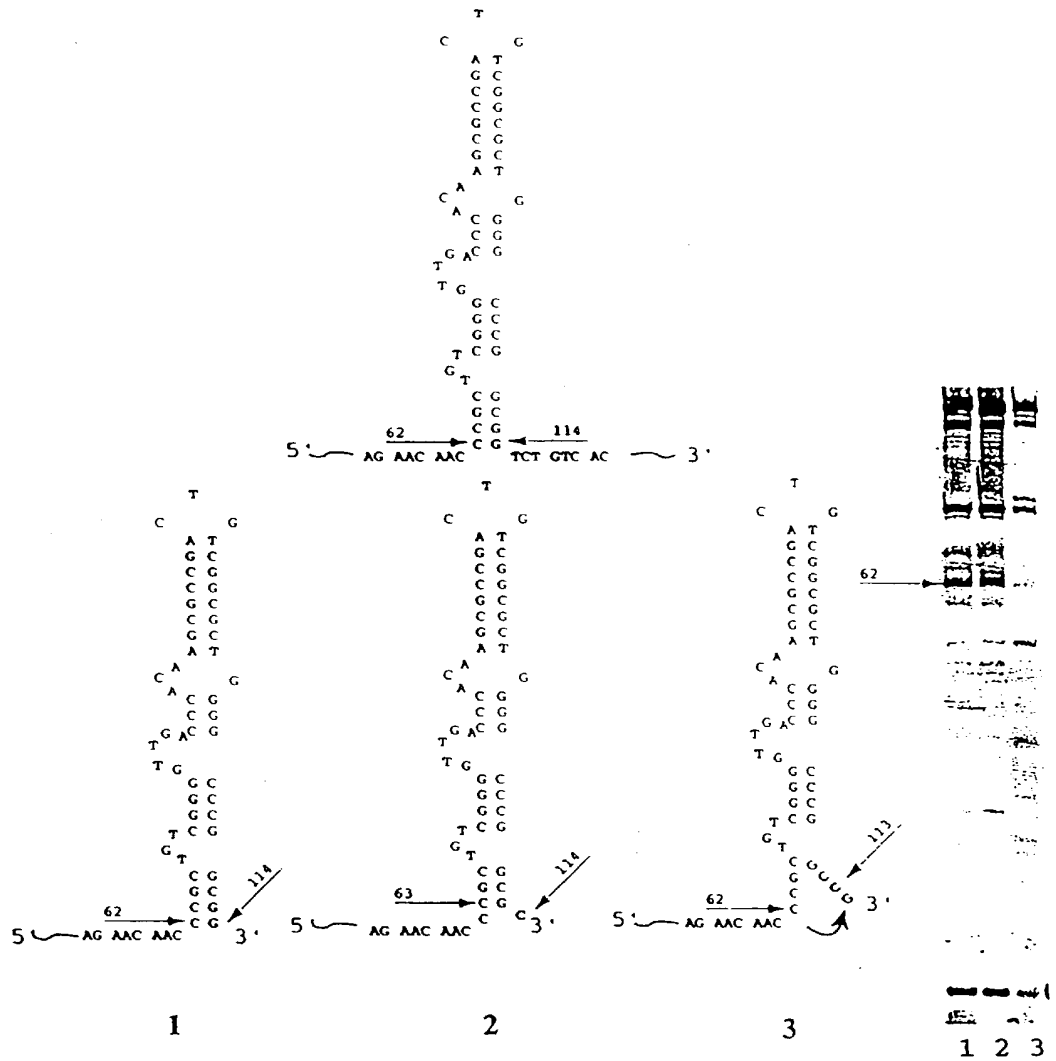
51/123

FIGURE 37A



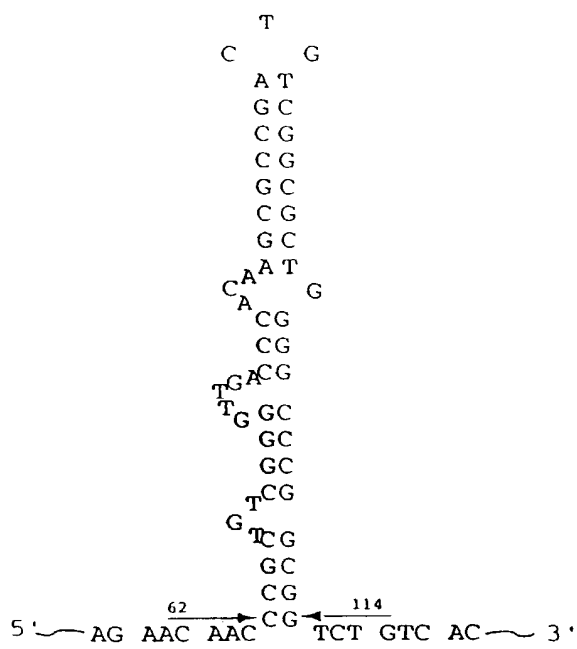
52/123

FIGURE 37B

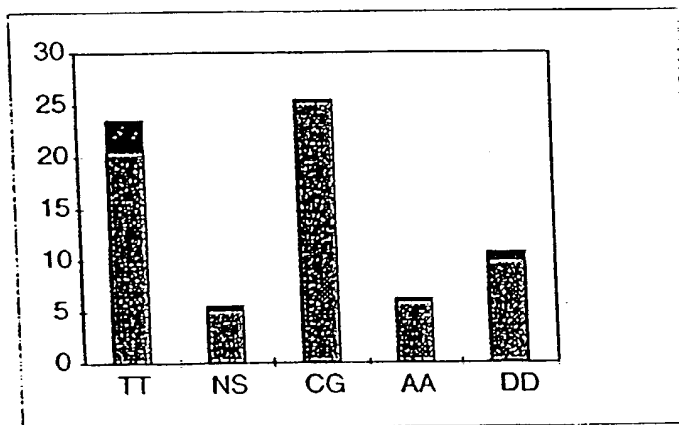


53/123

FIGURE 37C

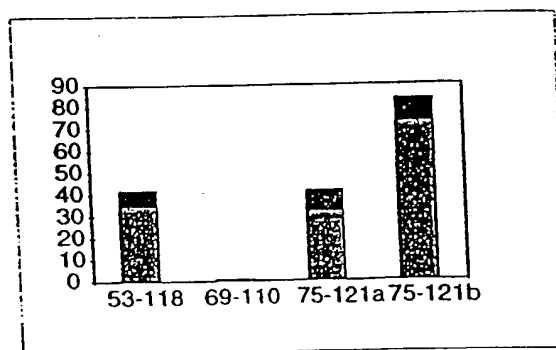
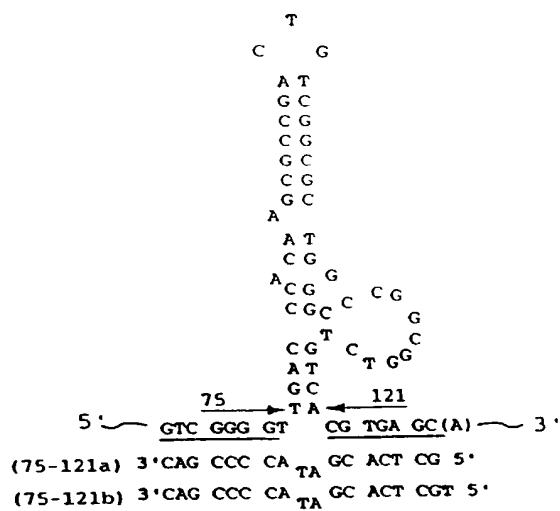
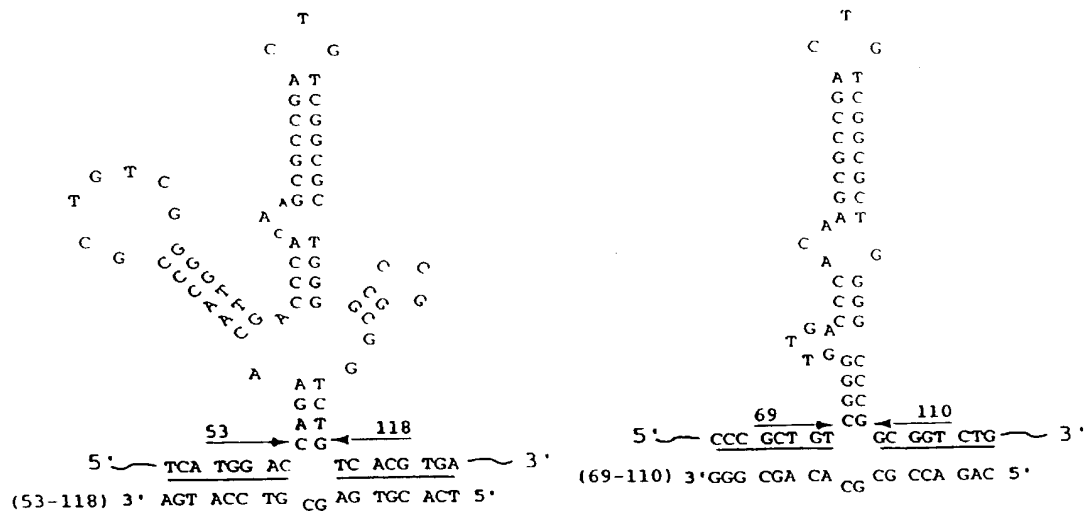


| | | | |
|----------|---------------|----|---------------|
| 62-114 a | 3' TCT TGT TG | TT | AG ACA GTG 5' |
| 62-114 b | TCT TGT TG | | AG ACA GTG |
| 62-114 c | TCT TGT TG | CG | AG ACA GTG |
| 62-114 d | TCT TGT TG | AA | AG ACA GTG |
| 62-114 e | TCT TGT TG | DD | AG ACA GTG |



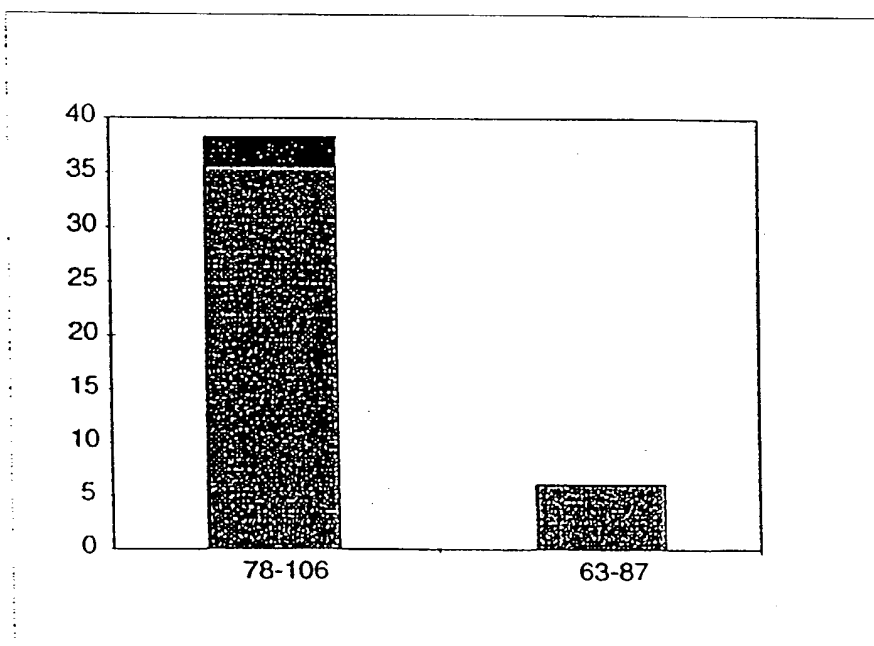
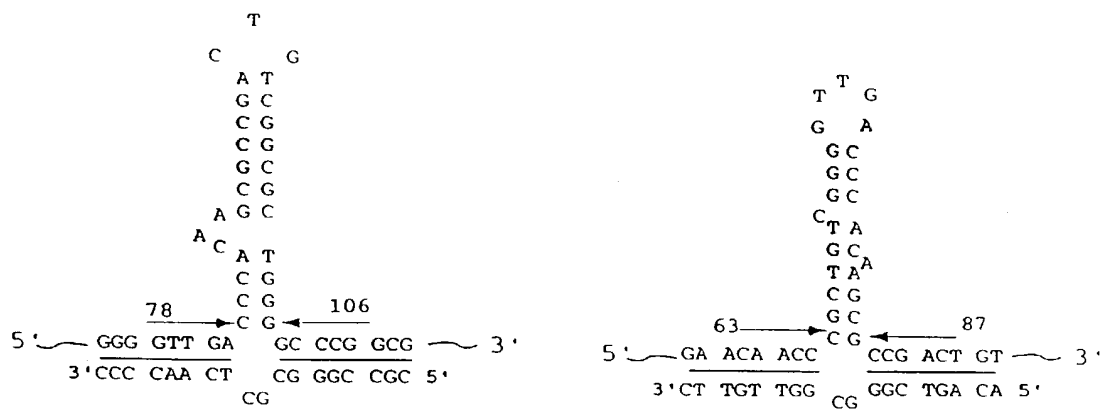
54/123

FIGURE 38A



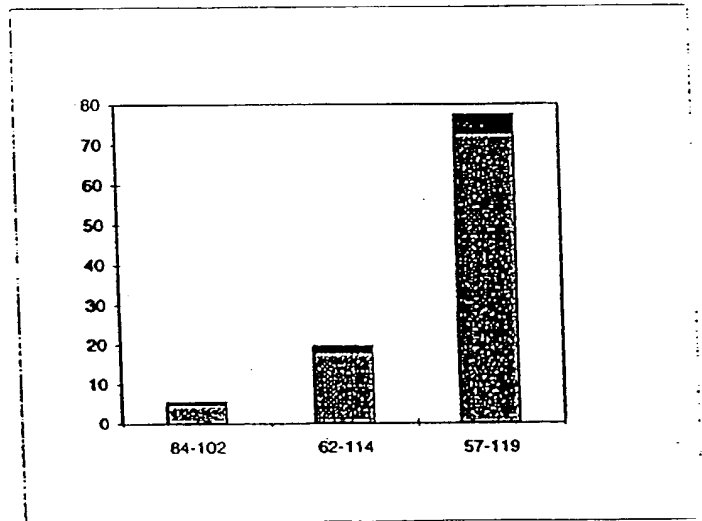
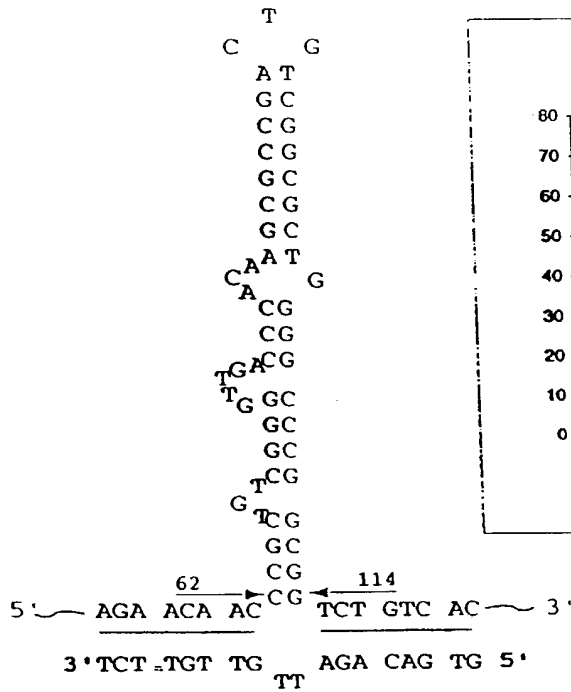
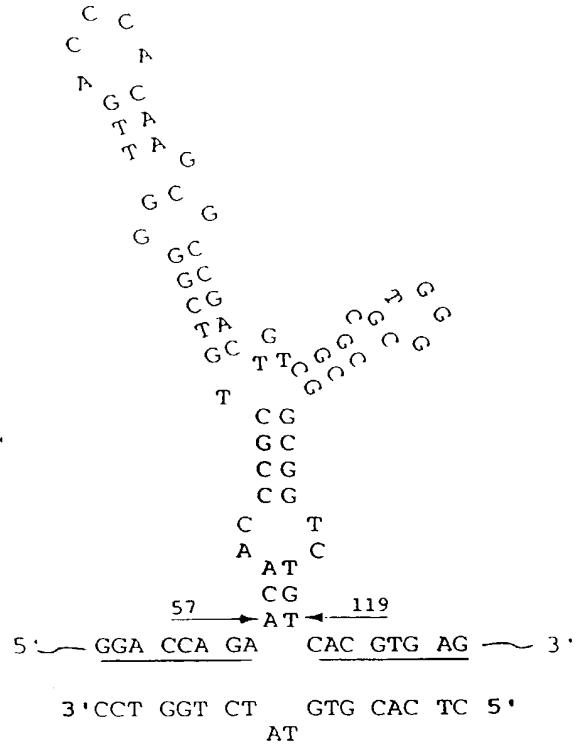
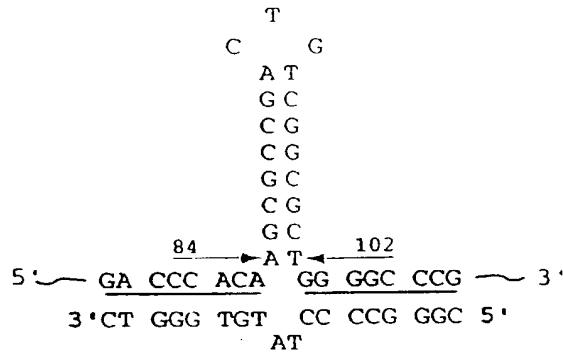
55/123

FIGURE 38B



56/123

FIGURE 38C



57/123

09822945.061501

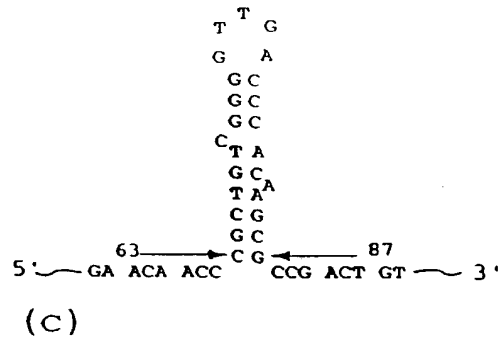
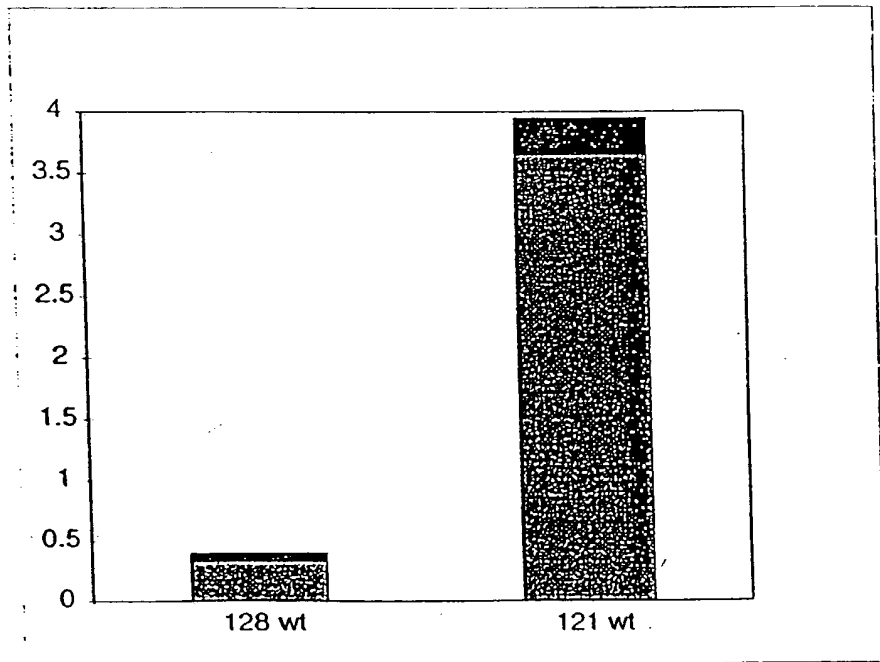
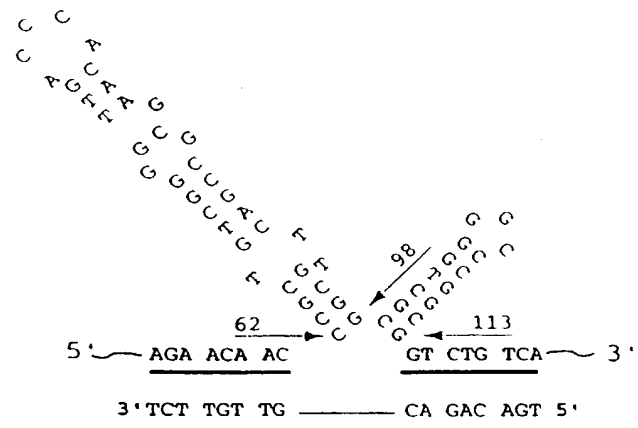
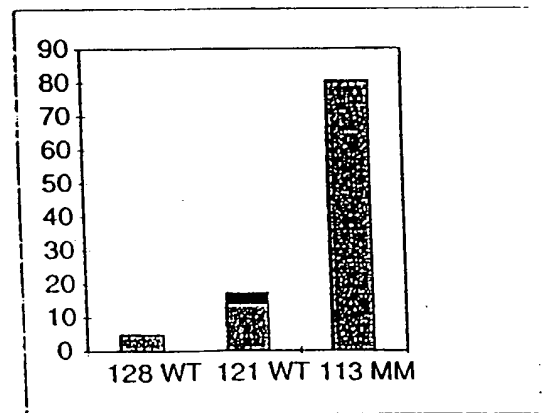
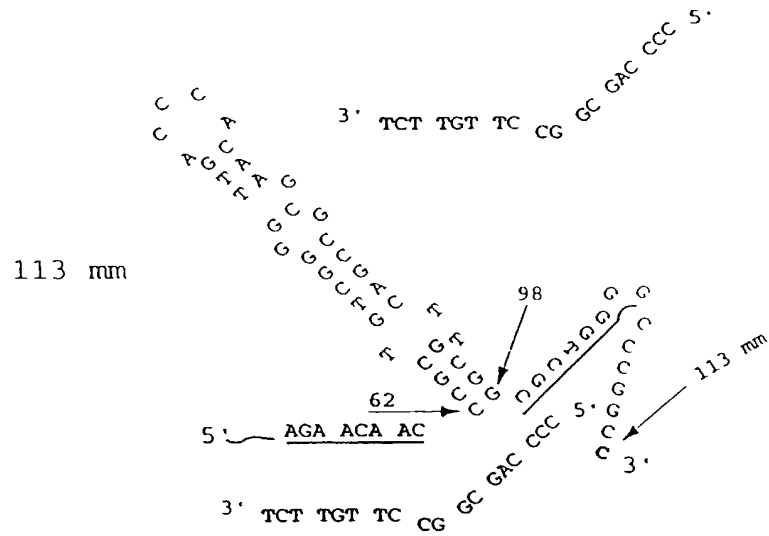
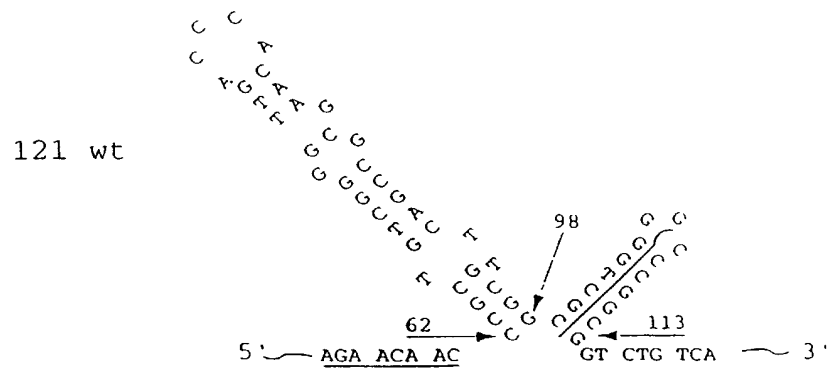
[illegible]
$$58/123$$

FIGURE 40



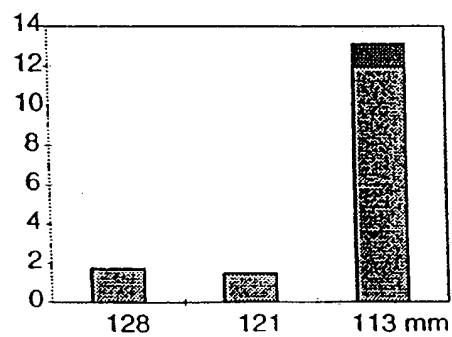
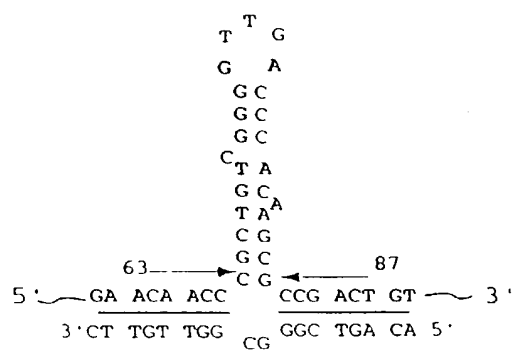
59/123

FIGURE 41



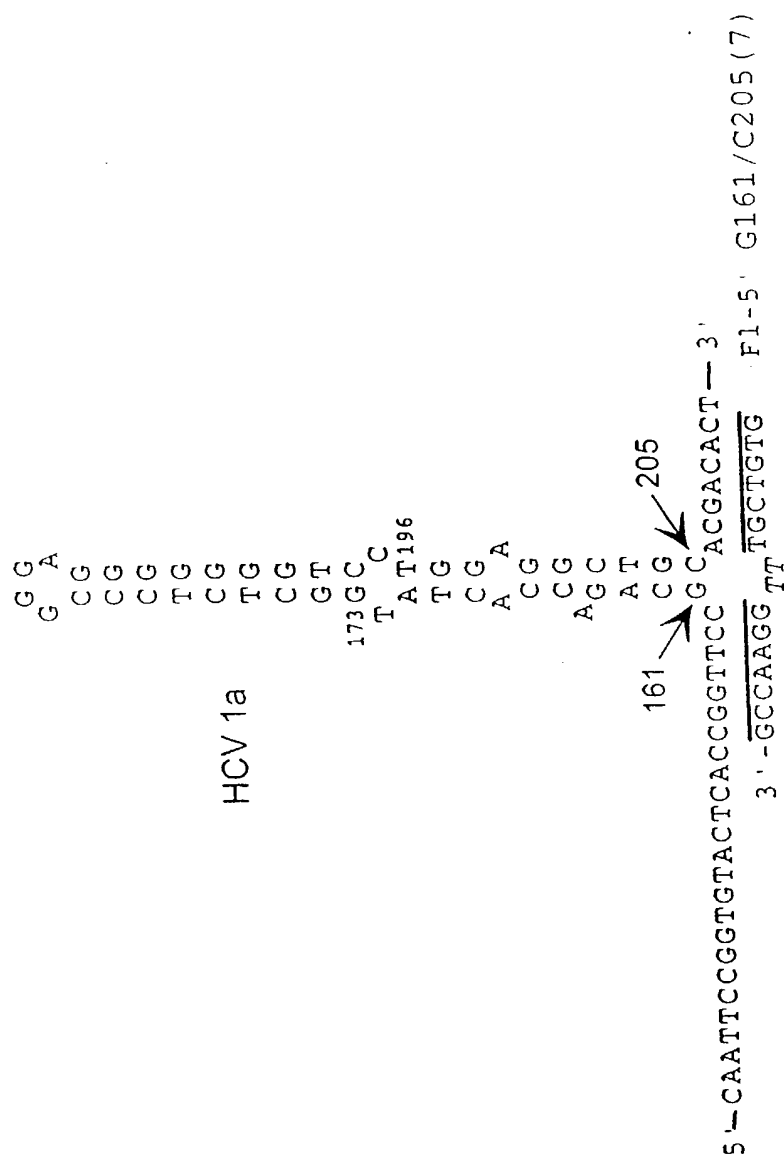
60/123

FIGURE 42



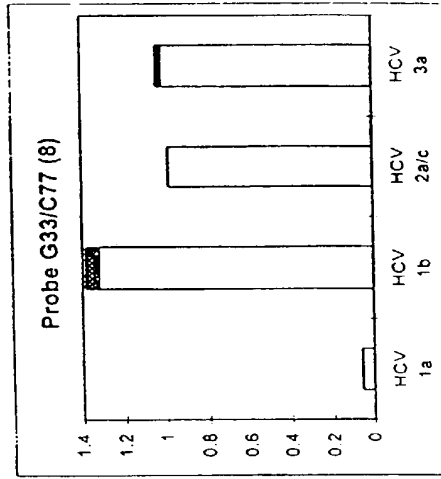
61/123

FIGURE 43A



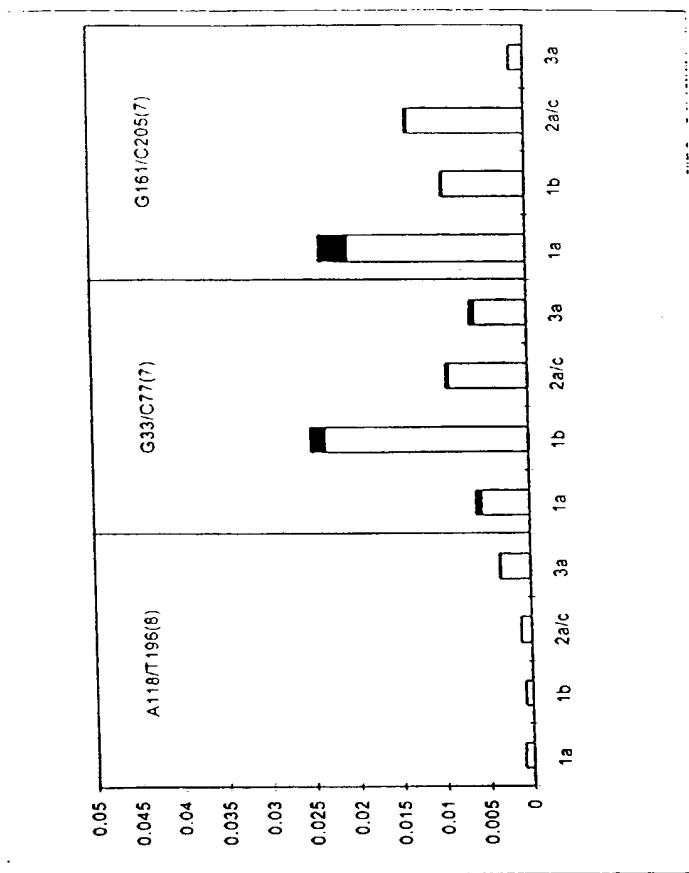
TEST NO. 54628860

FIGURE 44A

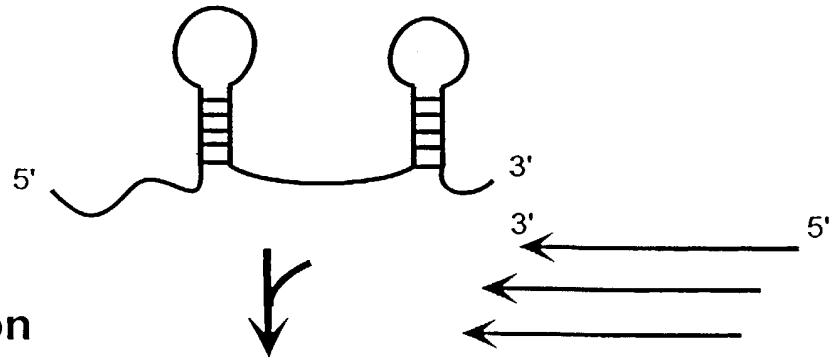


64/123

FIGURE 44B



I) Hybridization



II) Reverse Transcription

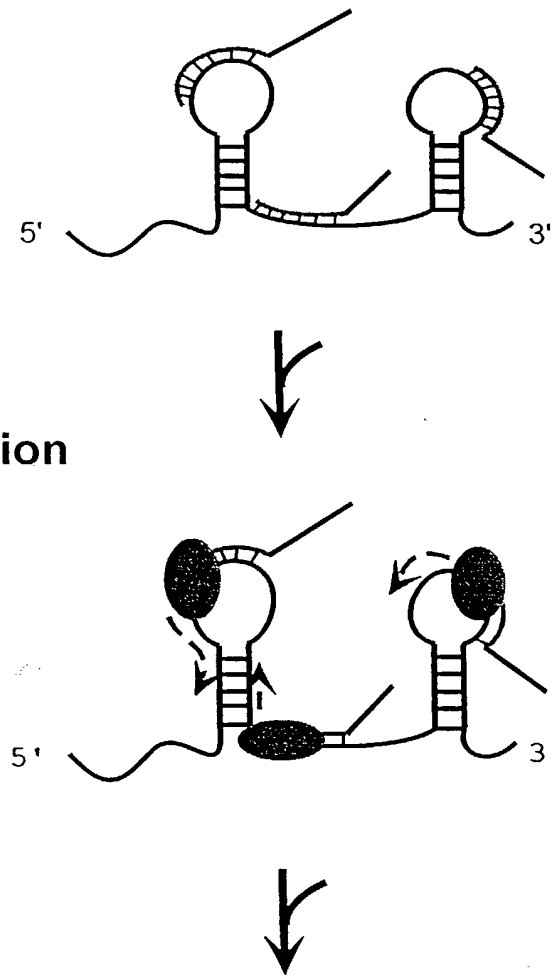


FIGURE 45A

66/123

| Table 1. Demographic characteristics of the study population | |
|--|-----------------|
| Age (years) | 50.0 ± 10.0 |
| Gender | |
| Male | 50.0% |
| Female | 50.0% |
| Education (years) | 12.0 ± 2.0 |
| Marital status | |
| Married | 80.0% |
| Single | 20.0% |
| Occupation | |
| Professional | 30.0% |
| Managerial | 20.0% |
| Technical | 10.0% |
| Skilled | 20.0% |
| Unskilled | 20.0% |
| Income (USD/month) | 1,500.0 ± 500.0 |
| Health status | |
| Good | 70.0% |
| Fair | 20.0% |
| Poor | 10.0% |

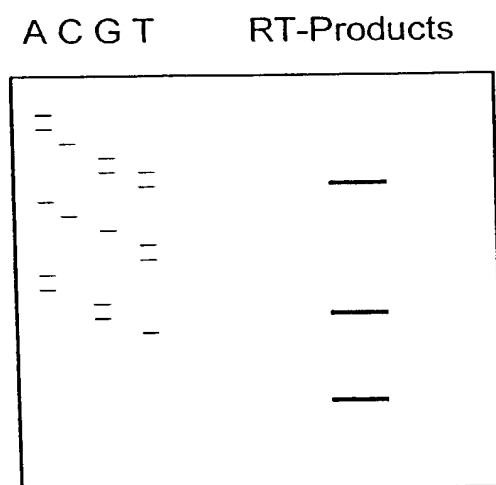
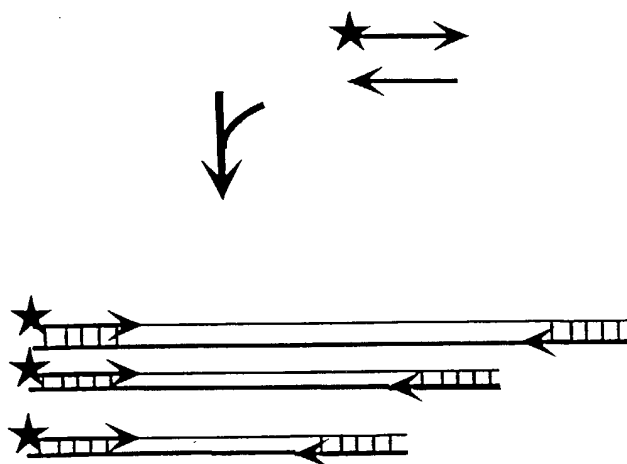
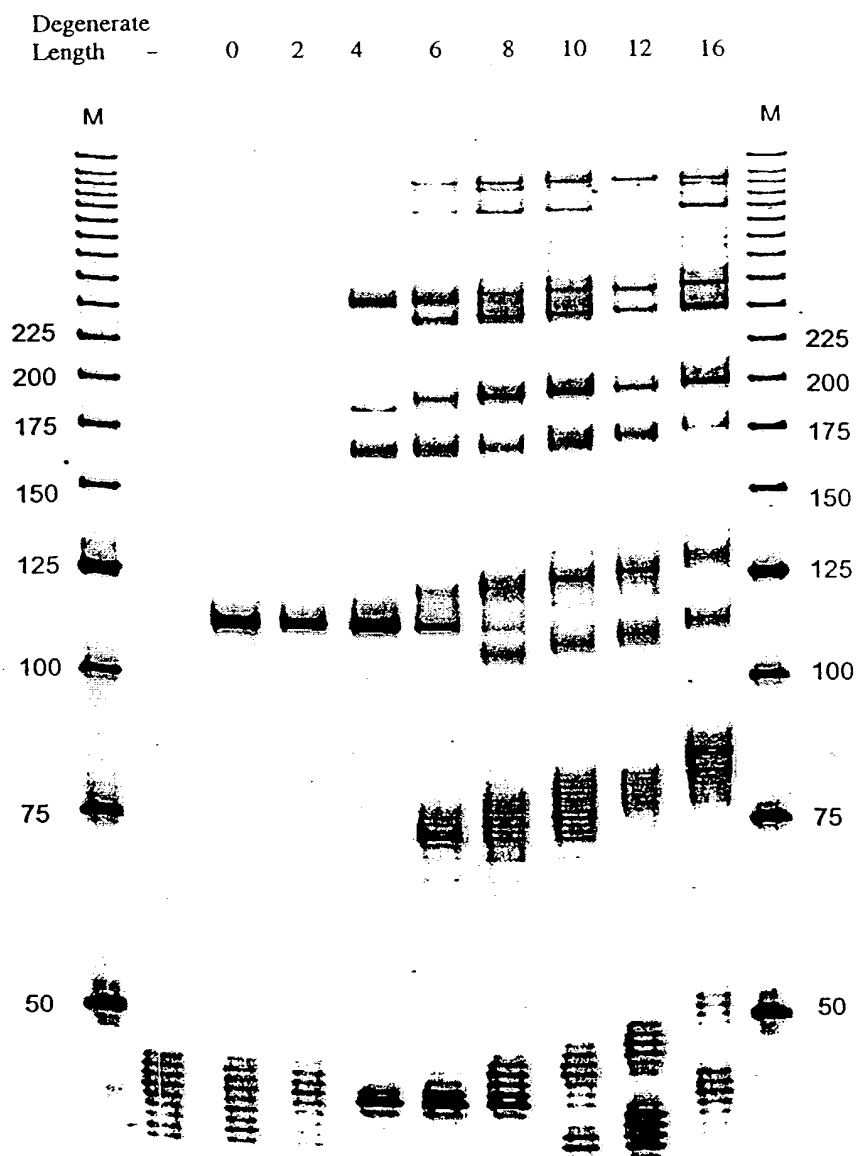


FIGURE 45B

$$67/123$$

FIGURE 46



68/123

09882945-061501

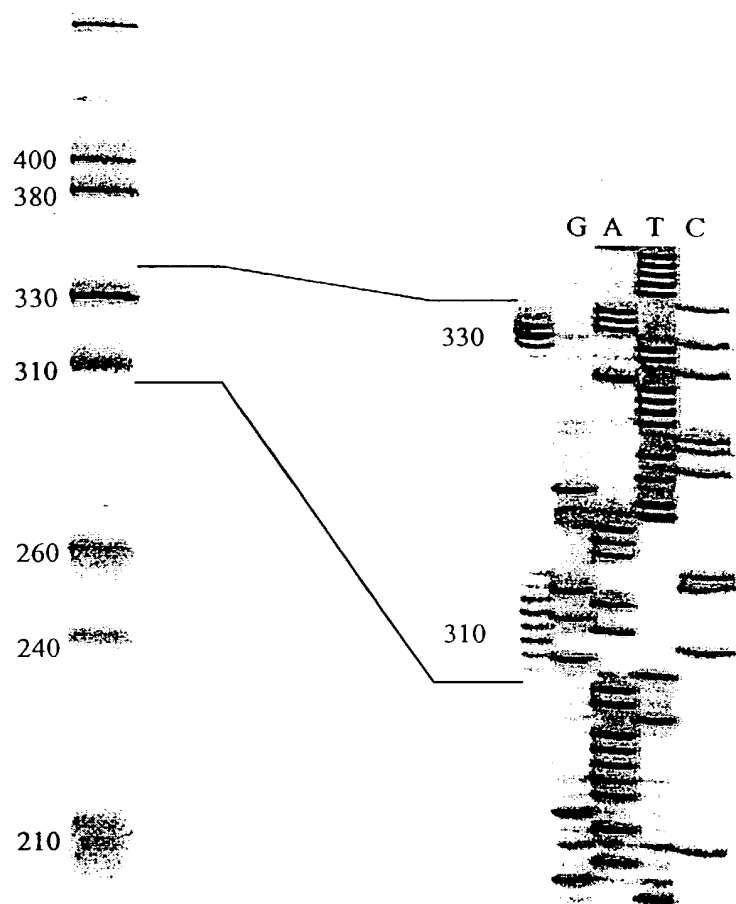


FIGURE 47

69/123

105FAD" 54628860

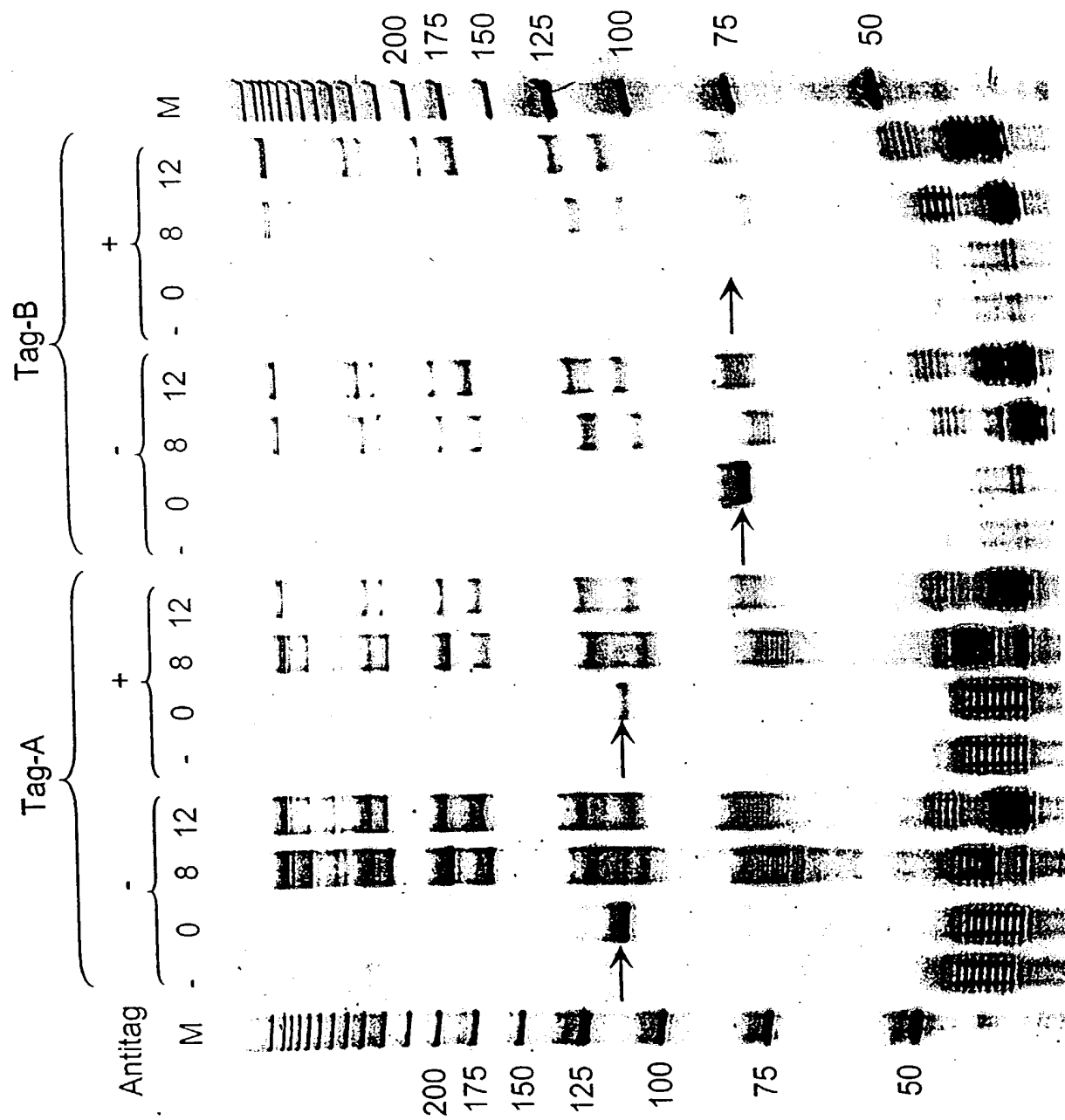


FIGURE 48

170/123

09882945-061501

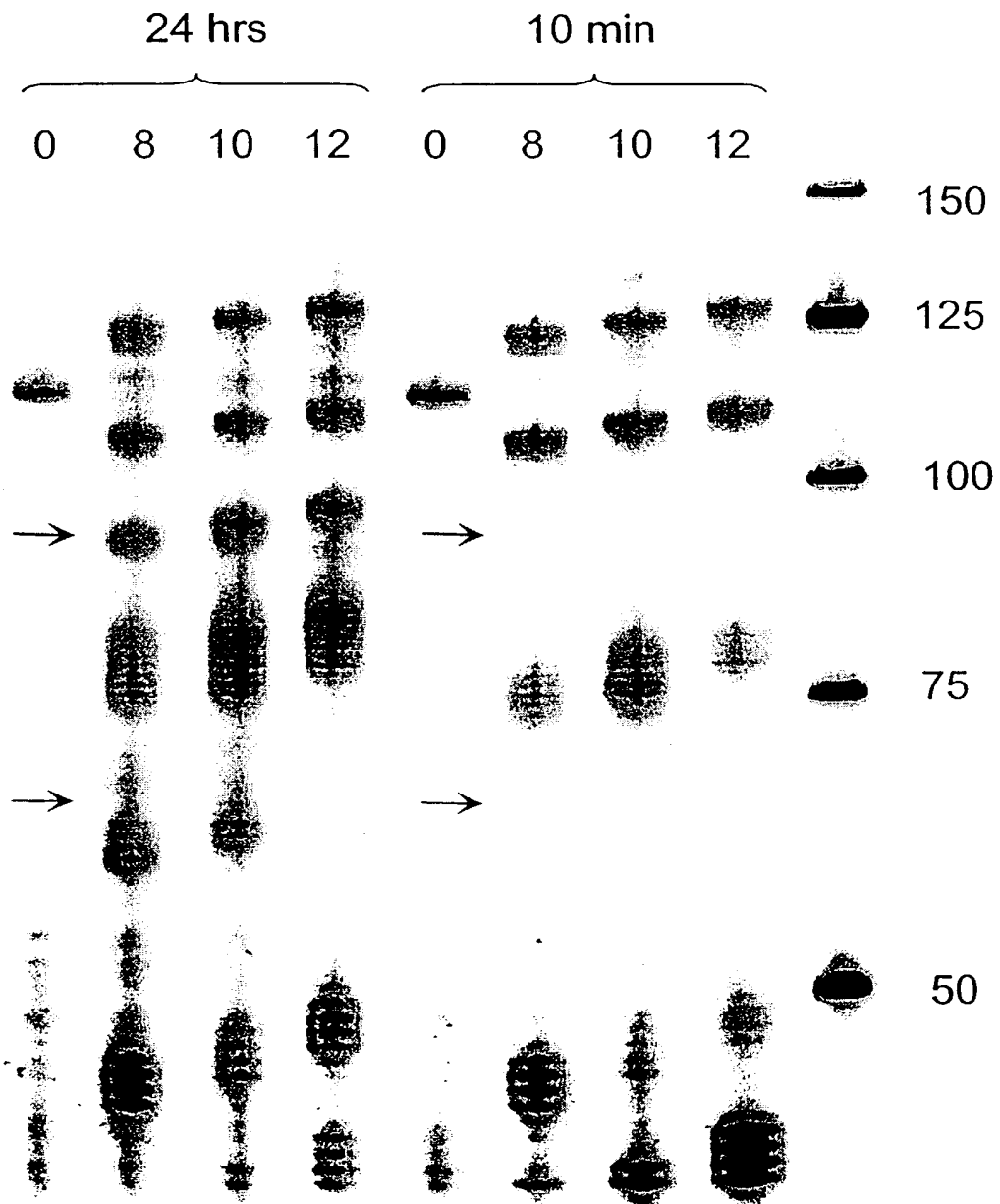
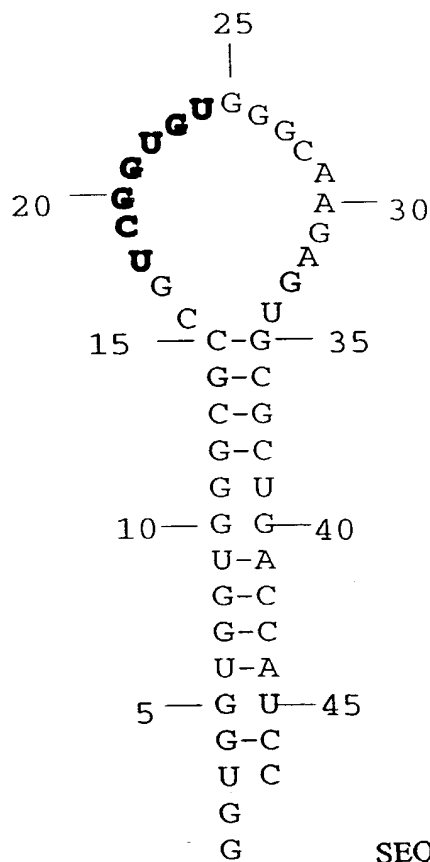


FIGURE 49

71/123

09882945.061501



SEQ ID 142

FIGURE 50A

72/123

09882945-05190-54628860

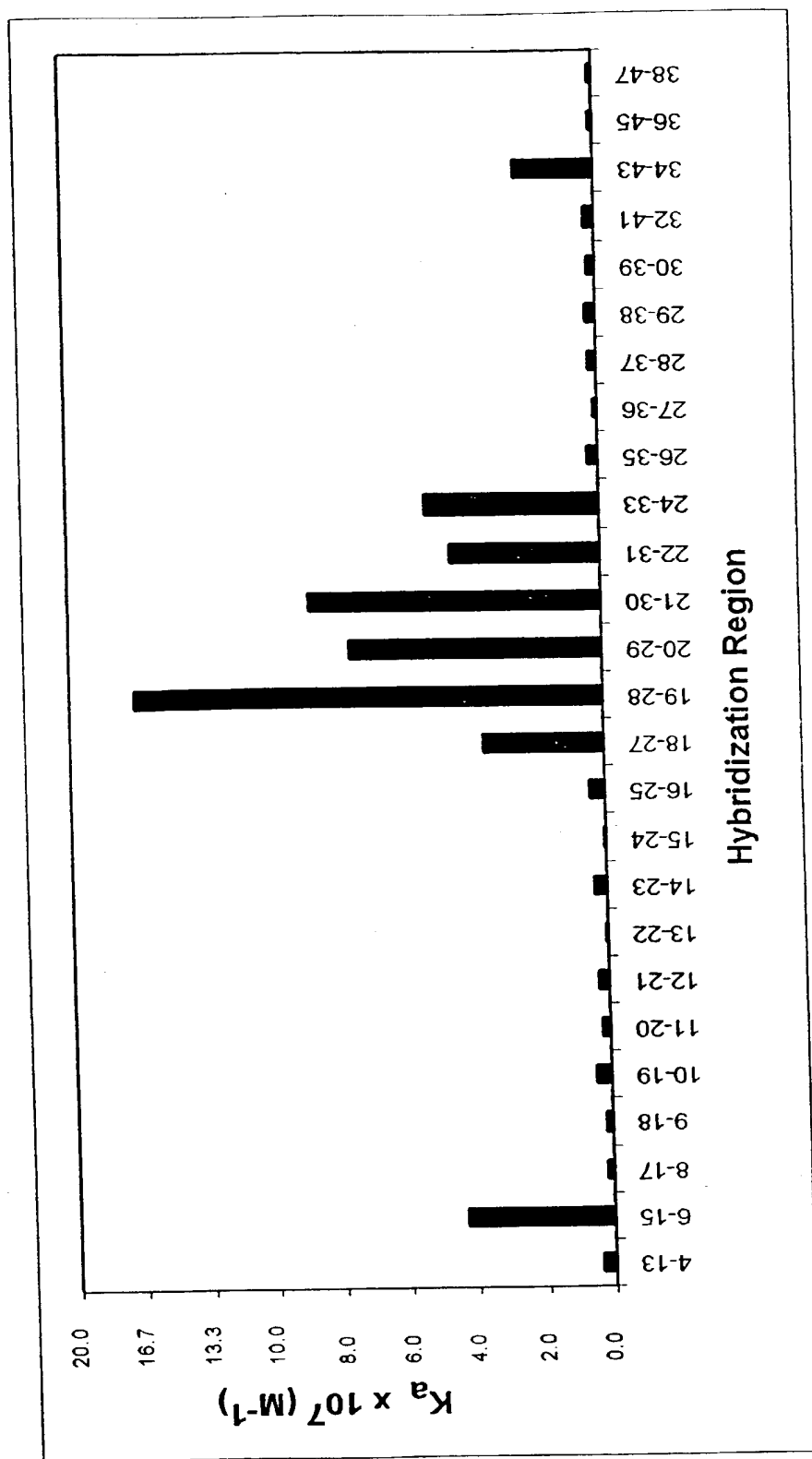


FIGURE 50B

73/123

FIGURE 51

1 ACACUUGCUU UUGACACAAC UGUGUUUACU UGCA**AAUCCCC** CAAAACAGAC

51 AGA**AUGGUGC** AUCUGUCCAG UGAGGAGA**AAG** **UCUGCGGUCA** CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

09862915.061501

74/123

FIGURE 52A

ISIS 1571(-) ISIS 3067(+)
1 GCGCCCC AGT CGACGCTGAG CTCCT CTGCT ACTCAGAGTT

ISIS 1570(+)
41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCCGGCC

81 CGCGCTGCCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC

121 CCAGGACCTG GCAATGCCCA GACATCTGTG TCCCCCTCAA

161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG

201 CAGCACCTCC TGTGACCAGC CCAAGTTGTT GGGCATAGAG

241 ACCCCGTTGC CTAAAAAGGA GTTGCTCCTG CCTGGGAACA

281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)
321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA

361 ACAGCTAAAA CCTTCCTCAC CGTGTACTGG ACTCCAGAAC

401 GGGTGGAACT GGCACCCCTC CCCTCTTGGC AGCCAGTGGG

441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA

481 CCCCGGGGCCA ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

0982245-061501
TOST 99-54628860

75/
123

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA

as 610

561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA

601 GCCAATTTCT **CGTGCCGCAC** TGA ACTGGAC CTGCGGCCCC

641 AAGGG**CTGGA** GCTGTTTGAG AAC**ACCTCGG** CCCCCTACCA

681 GCTCCAGACC TTTGTC**TGC** **CAGCGACTCC** CCCACA ACTT

721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG

761 TGGTCTGTTC CCT**GGACGGG** CTGTTCCCAG TCT**CGGAGGC**

801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC

841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT

881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT

921 GACGTGTGCA GTAATACTGG GGAACCAGAG **CCAGGAGACA**

961 CTGCAGACAG **TGACCATCTA** CAGCTTTCCG GCGCCCAACG

1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

09022945-061501

176/123

JRE 52C

1041 GACAGTGAAG TGT**GAGG**CCCC ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGG**CGCAG

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTAT**G**

1241 **GCCCCC**GACT GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATT**CCCAGC** AGACTCCAAT GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTTT**TTCC** ACTGCCCATC **GGGGAATCAG** TGA**CTGTCAC**

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CTGCAGGCCT **CAGCACGTAC**

0982945.061501

77/123

FIGURE 52D

1561 CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC

as 1630 as 1630h(+++)

1601 AACAGGCCCA AAAAGGGACC CCCATGAAAC CGAACACACA

ISIS 1938 (+)

1641 AGCCACGCCT CCCTGAACCT ATCCCGGGAC AGGGCCTCTT

1681 CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCTACCGG

1761 CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 TACAACAGCA TTTGGGGCCA TGGTACCTGC ACACCTAAAA

1841 CACTAGGCCA CGCATCTGAT CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA

1961 CATAGCCCCA CCATGAGGAC ATACAACTGG GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA

2041 CAGAAGAAGT GGCCCTCCAT AGACATGTGT AGCATCAAAA

0982045-061501

78/123

URE 52E

ISIS 2302 (+)

2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTTTACCAG CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGG TTCAGAG ATTACCCAGT

2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT

2481 GTTAGCCACC TCCCCACCCA CATACATTTTC TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGAATATG CCCAAGCTAT GCCTTGTCTCT CTTGTCCTGT

09882945-061501

179/123

URE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

0982045-061501

80/123

0968645-064504

81/123



53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG

site 560

521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC

site 570

561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG

601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC

641 UACAAUAUUU GAAUUUUAAA UCUAAAUCUA UUUUAUAAUA

681 UUAACAUAU UUAUAUUGGG GAAUAUAUUU UUAGACUCAU

721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG

761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUUAU UUAUAAUCC

801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA

site 850

site 860

site 880

841 CUAUUUAGGC AAGGCUAUGU GAUACAAGG CUUUAUCUCA

site 890

site 910

881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG

921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUUAU

961 AAGUGAAGUG AUACUAUCCA GUUACUA

09882945.061501

82/123

FOST90" 54628860

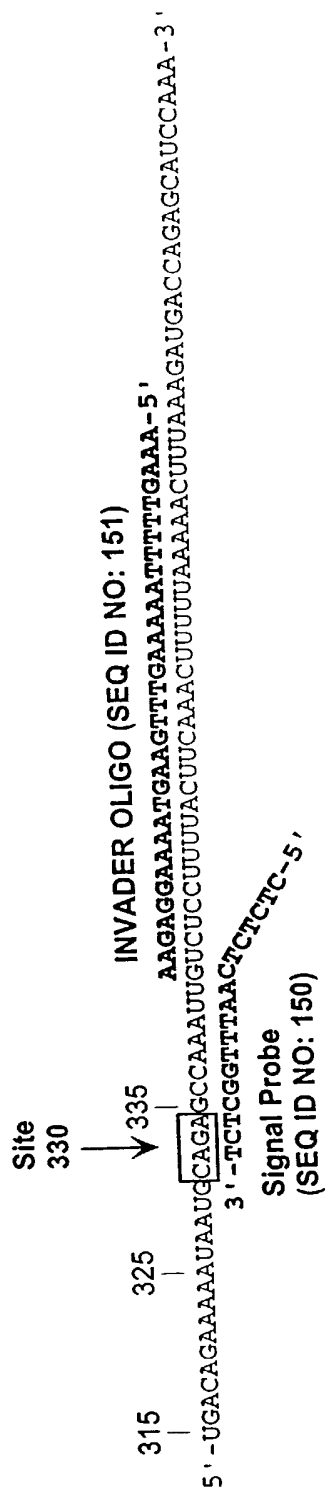
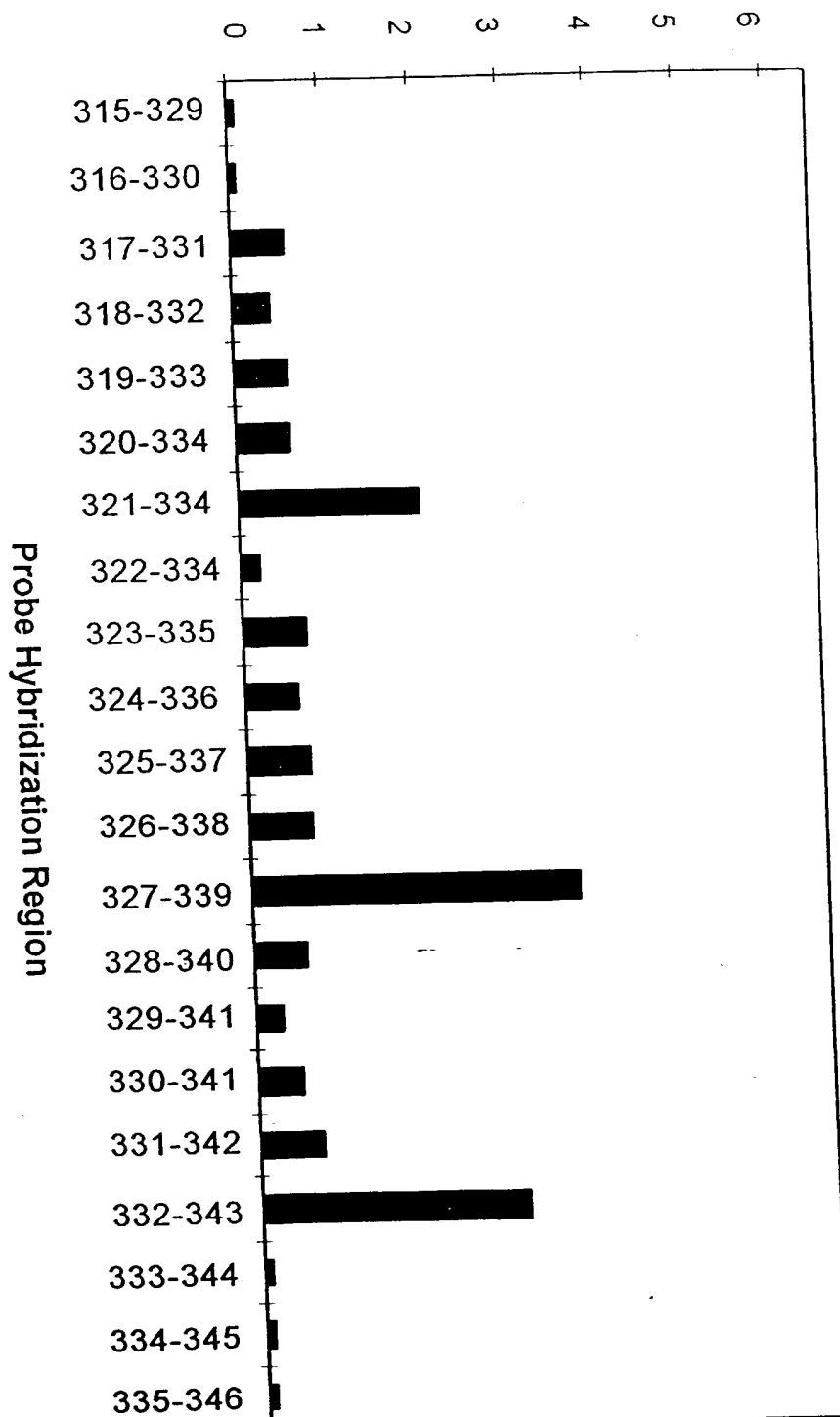


FIGURE 54A

83/123

Turnover Rate (min^{-1})



84/123

FIGURE 54B
09882945.061501

FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUA GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUU AUAAUACAGU AGCAACCCUC UAUUGUGUGC

1060 AUCAAAGGAU AGAGAUAAAA GAC**CCAAGG** AAGCUUUAGA CAAGAU**AGAG**

85/123

0982945-061501

FIGURE 55B

1110 **GAA**GAGCAAA ACAAAGUAA GAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGG**ACACAGC AAUCAGGUCA GCCAAAUUA CCCUAUAGUG CAGAACAUC

Primer 5

1210 **AGGGG**CAAAU GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGAA**GGAG** **CC**ACCCACACA AGAUUUAAAC ACCAUGC

1360 ACACAGUGGG GGGACAUCAA **GC**AGCCAUGC AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUG**AGGAAG CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGC**ACCA** GGCCAGAUGA GAGA**ACCAAG** **GG**GAAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCAGUAG GAGAAAUUUA UAAAAGAUUG AUAAUCCUGG GAUUAUUAA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCC**GAGCAAG CUUC**ACAGGA** GGUAAAAAU **UGG**AUGACAG AAACCUUGUU

86/123

0988345.061504

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGCGGCUAC** ACUAGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGAGGA

1860 CCCGGCCAUU AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUAUUGAUGC **AGAGAGGCAA** UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGAAG **GGCACACAGC** CAGAAAUUGC

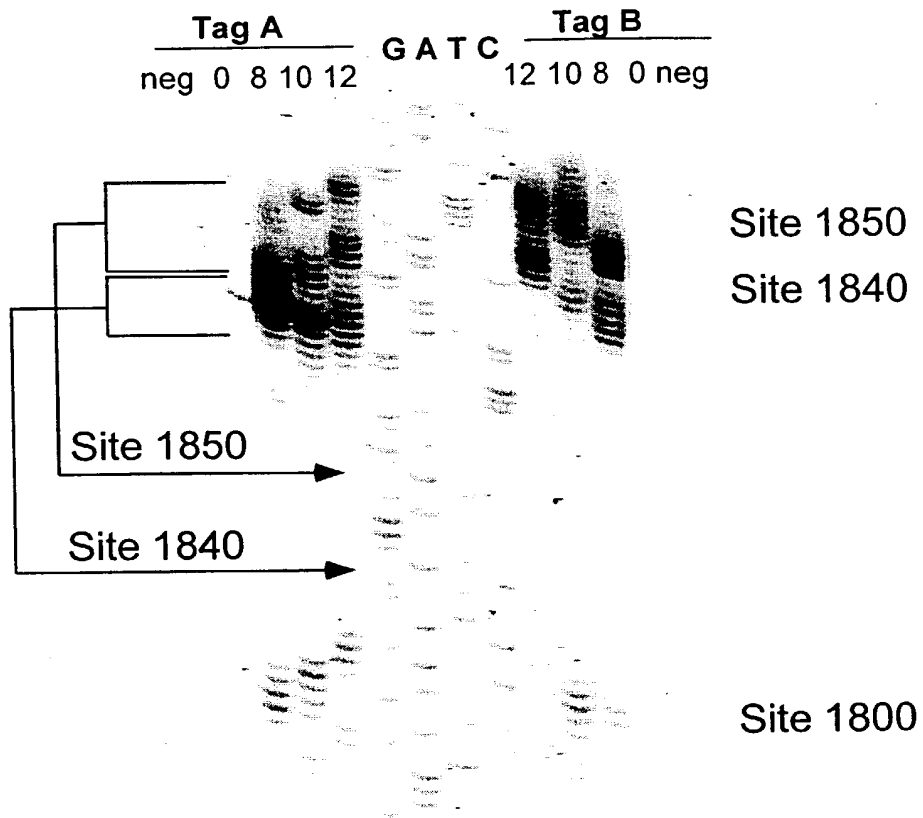
2010 AGGGCCCCUA GGAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

0902045 061501

87/123

FIGURE 56

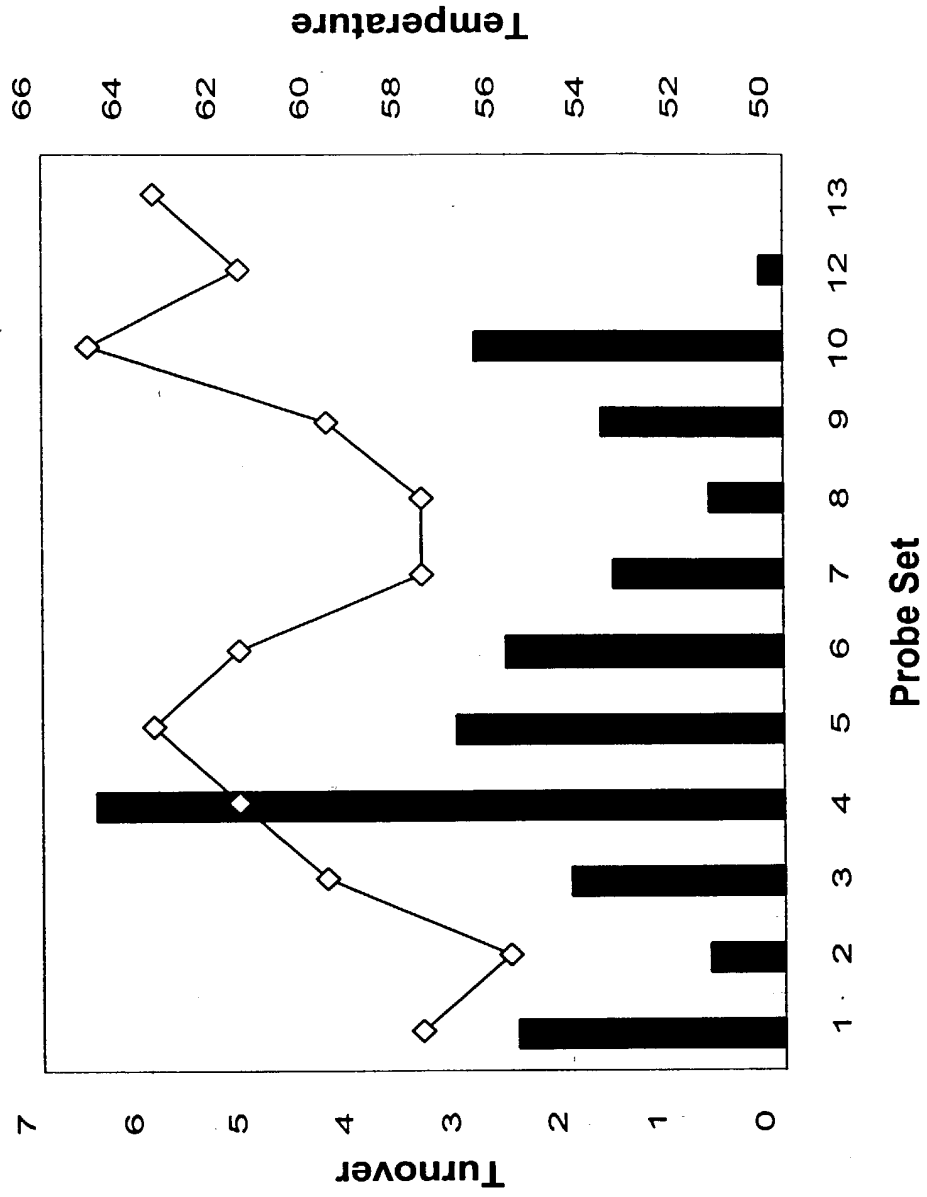


88/123

FIGURE 57

| | | |
|---|--------------------------------|-------|
| (SEQ ID NO:188) | CGTATTCGTTCTCAAAACCGACTTGCT-5' | 13 |
| (SEQ ID NO:187) | AGGTATTCGTTCTCAAAACCGACT | 12 |
| (SEQ ID NO:186) | ACGGTATTCGTTCTCAAAACCGAC | 10=11 |
| (SEQ ID NO:185) | CCCGGTATTCGTTCTCAAAACCGA | 9 |
| (SEQ ID NO:184) | CGCCGGTATTCGTTCTCAAAACCG | 8 |
| (SEQ ID NO:183) | CGCCGGTATTCGTTCTCAAAACCG | 7 |
| (SEQ ID NO:182) | AGGCCGGTATTCGTTCTCAAAAC | 6 |
| (SEQ ID NO:181) | ATGGCCGGTATTCGTTCTCAAAAC | 5 |
| (SEQ ID NO:180) | ACTGGCCGGTATTCGTTCTCAAA | 4 |
| (SEQ ID NO:179) | ACCTGGCCGGTATTCGTTCTCAA | 3 |
| (SEQ ID NO:178) | ATCCTGGCCGGTATTCGTTCTCA | 2 |
| (SEQ ID NO:177) | ACTCCTGGCCGGTATTCGTTCTC | 1 |
| 5'-CAUGCAGGAGUAGGAGACCCGCCAUAAGCAAGUUUGGCUAAGCAAUGAG-3' | (SEQ ID NO:158) | |
| 1 CAGTCCCTCATC | (SEQ ID NO:164) | |
| 2 AGTCCCTCATCC | (SEQ ID NO:165) | |
| 3 GTCCCTCATCCT | (SEQ ID NO:166) | |
| 4 TCCCTCATCCTC | (SEQ ID NO:167) | |
| 5 CCTCATCCTCC | (SEQ ID NO:168) | |
| 6 CCTCATCCTCCT | (SEQ ID NO:169) | |
| 7 CTCATCCTCCTG | (SEQ ID NO:170) | |
| 8 TCATCCTCCTGG | (SEQ ID NO:171) | |
| 9 CATCCTCCTGGG | (SEQ ID NO:172) | |
| 10 ATCCTCCTGGG | (SEQ ID NO:173) | |
| 11 TCCTCCTGGG | (SEQ ID NO:174) | |
| 12 CCTCCTGGG | (SEQ ID NO:175) | |
| 13 CTCCTGGGCGAAA-FL-5' | (SEQ ID NO:176) | |

FIGURE 58



90/123

FIGURE 59

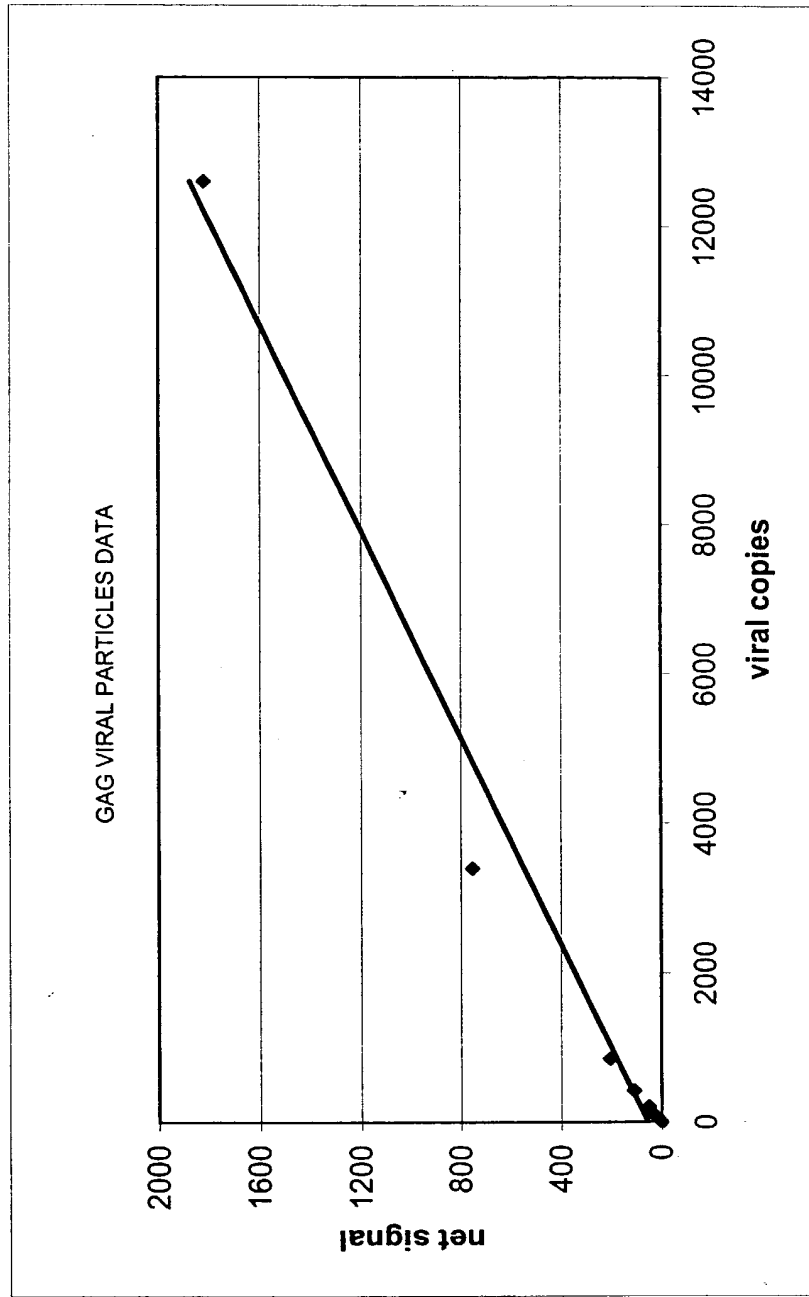
(SEQ ID NO:180)
 ACTGGCCCGGTATTCCGTTCTCAAA
 5' -CAUGUAGGGAGUAGGAGGACCCGGCCCAUAAGGCAAGAGUUUUGGCUGAAGCAAUGAG-3'
 (SEQ ID NO:158)
 TCCCTCATCCTCCTCCGCACTGCC-5'
 (SEQ ID NO:189)

5' -AGGAGTAGGAGGAGG-3'
 (SEQ ID NO:190)

(SEQ ID NO:191) (SEQ ID NO:193)
 5' -CCGTCACGCCTCC
 3' -TGGCAGTCCGGAGGTTGACGAAGAGGC-5'
 (SEQ ID NO:192)

Diagram showing a sequence alignment with a mutation site marked by a circle 'Q' and a circle 'F' with arrows pointing to the corresponding positions in the sequences above.

FIGURE 60



92/123

FIGURE 61A

SEQ ID NO:159

primer 1
 3300 AGCUGGACUG UCAAUGACAU ACAGAAGUUA **GUGGGGAAAU UGAAUUGGGC**
 3350 AAGUCAGAUU **UACCCAGGGA** UUA**AAGUAAG** GCAAUUAUGU AAACUCCUUA
 3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG
 3450 CUAGA**ACUGG** CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU
 primer 2
 3500 GUAUUAUGAC CCAUCAAAAG ACUUAUAGC AGAAAU**ACAG** **AAGCAGGGGC**
 3550 **AAGGCCAAUG** GACAUAUCAA AUUUAU**CAAG** AGCCAUUUAA AAAUCUGAAA
 3600 ACAGGAAAAU AUGCAAGAAU **GAGGGGUGCC** CACACUAAUG AUGUAAAACA
 3650 AUUAACAG**AG** **GCAGUGCAAA** AAUAUACCAC AGAAAGCAUA GUAAUAUGGG
 primer 3
 3700 GAAAGACUCC UAAAUUUAAA CUGCCCAUAC AAAAGGAAAC AUGGGAAACA
 3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU
 3800 UAAUACCCCU CCCUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA
 3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGAUG **GGGCAGCUAA** **CAGGGAGACU**
 primer 4
 3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

0982945-061501

93/123

FIGURE 61B

3950 CACCCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC

4000 UAGCUUUGCA GGAUUC**CGGGA** UUAGAAGUAA ACAUAGUAAC AGACUCACAA

4050 UAUGCAUUAG GAAUCAUUA **AGCACAA**CCA GAUCAAAGUG AAUCAGAGUU

primer 5
4100 AGUCAAUCAA AUAUA**GAGC** AGUUAUAAA AAAGGAAAAG GUCUAUC**UGG**

4150 **CAUGGGUACC** AGCACACAAA GGA**AUUGGAG** GAAAUGAACA AGUAGAUAAA

4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGA**UAA**

4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAU**UGGAGA** GCAAUGGCUA

primer 6
4300 GUGAUUUUAA CCUGCCACCU GUAGUAGCAA AAGAAU**AGU** **AGCCAGCUGU**

4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG

4400 UCCAGGAAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC

4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUA UAG**AAGCAGA** AGUUAU**UCCA**

primer 7
4500 GC**AGAA**CAG **GGCAGG**AAAC AGCAUAUUUU CUUUUAAAAU **UAGCAGGAAG**

4550 **AUGGCCAGUA** AAAACAAUAC AUAC**UGACAA** **UGGCAGCAAU** UUC**ACCGGUG**

4600 CUACGGUUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** **GGAAUUUGGA**

94/123

0982945-061504

FIGURE 61C

4650 AUUCCCUACA AUCCCCAAG UCA**AAGG**AGUA GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAGGAC AGGUAAGAGA **UCAGGC**UGAA CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAA**AGAAUA GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUAC AAAAACAAAU UACAAAAAUU CAAAUUUUC

primer 9

4900 GGGUUUAUUA CAG**GGAC**AGC AGAAAUCCAC UUUGGA**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGAU AUAGUGACAU

5000 AAAAG**UAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

0982945 061501
TOST 90 5462860

95/123

FIGURE 63

5 3'-TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:213)
 6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:214)
 5'-GAAAGGACCAGCAAAGCUCUCUGGAAAGGUAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3' (SEQ ID NO:209)
 4930 ACCCGTCATCATTTATGTTCTATTATCACTGTATTTT-5' 5
 6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:210)
 5'-GAAAGGACCAGCAAAGCUCUCUGGAAAGGUAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3' (SEQ ID NO:210)
 4960 CTTTCCACTTCCAAA-5, (SEQ ID NO:206)
 5 CTTTCCACTTCCAAA-5, (SEQ ID NO:205)
 4960 CTTTCCACTTCCAAA-5, (SEQ ID NO:205)
 7 3'-TCGAGGAGACCTTTCCAC (SEQ ID NO:215)
 8 3'-TCGAGGAGACCTTTCCACT (SEQ ID NO:216)
 5'-GAAAGGACCAGCAAAGCUCUCUGGAAAGGUAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3' (SEQ ID NO:211)
 4930 TCCCCCGTCATAAAA-5, (SEQ ID NO:208)
 7 TCCCCCGTCATAAAA-5, (SEQ ID NO:207)
 4960 TCCCCCGTCATAAAA-5, (SEQ ID NO:207)

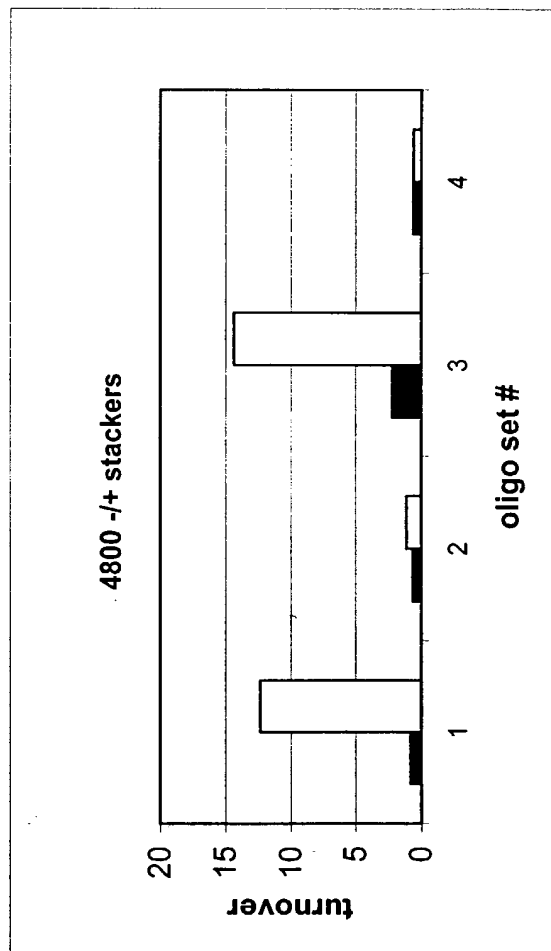
FIGURE 64

1 4790 4810 (SEQ ID NO:224) (SEQ ID NO:221)
3'-TCCCCCCTAACCCCCCATG ATTTCATTATCTGTATTATCGTTGTCTGTATGT-5'
5'-AAGAAAGGGGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAACU-3'
(SEQ ID NO:159)
TCACGTCCCCAAA-5,(SEQ ID NO:217)

2,4 4790 4810 (SEQ ID NO:225) (SEQ ID NO:222)
3'-CTGTCGTATGTTTACCGTCATAAGTAGGT ACCCTAACCCCATGTCTAC-5'
5'-AGACAGCAGUACAAAUAGGCAGUAUUAUCCACAAUUUUAAAAGAAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAG-3'
(SEQ ID NO:159)
GTTAAATTTTCTTTTCCCCTATATA-5,(SEQ ID NO:220)
GTTAAATTTTCTTTTCCCCTATATA-5,(SEQ ID NO:218)

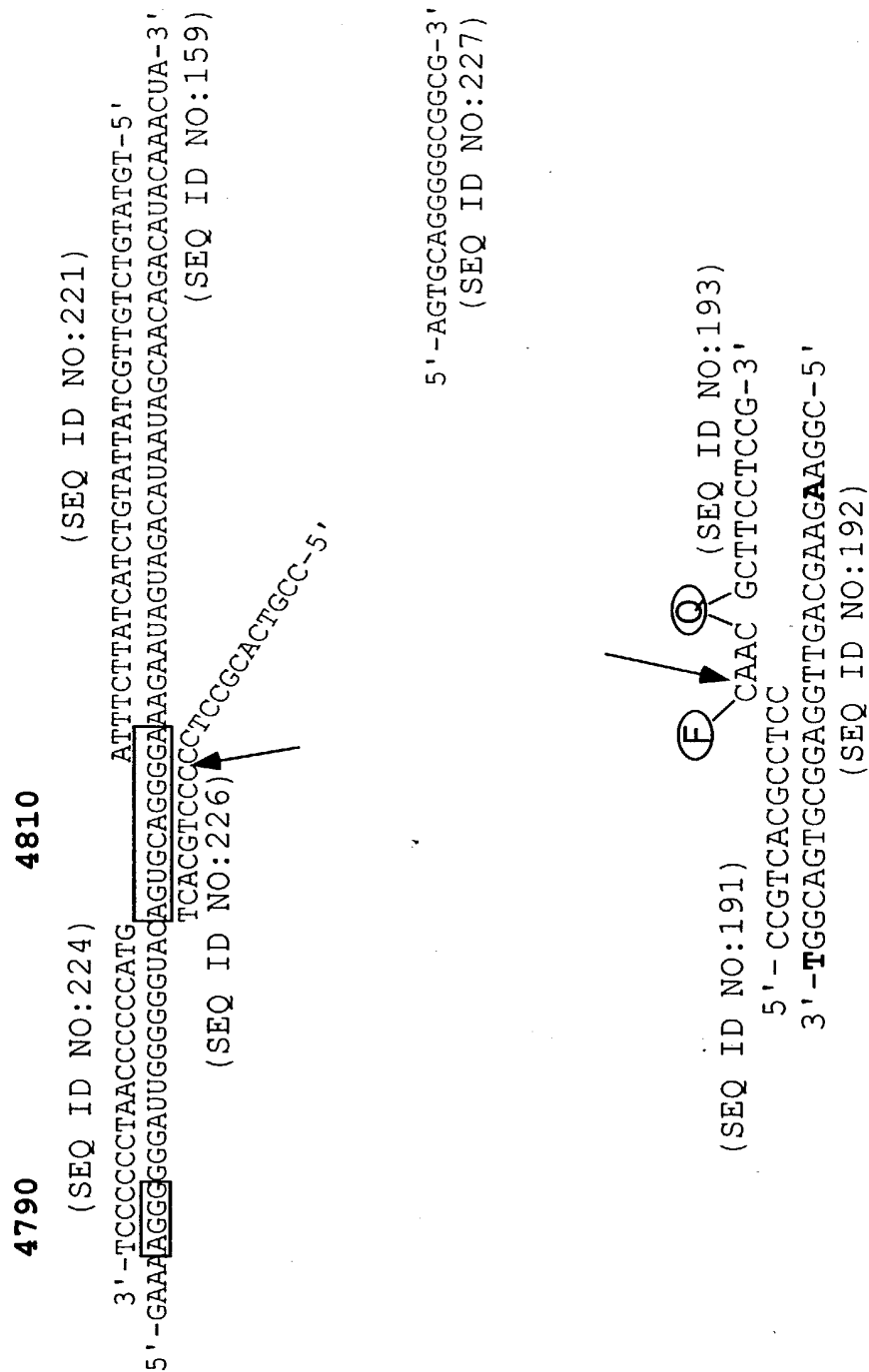
3 4790 4810 (SEQ ID NO:222) (SEQ ID NO:223)
ACCCCTAACCCCCCATGTCTAC-5' CATCATCTGTATTATCGTTGTCTGTATGTTGATTTC
5'-AAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAACUAAAGAA-3'
(SEQ ID NO:159)
GTCCCCCTTTCTTAAA-5,(SEQ ID NO:219)

FIGURE 65



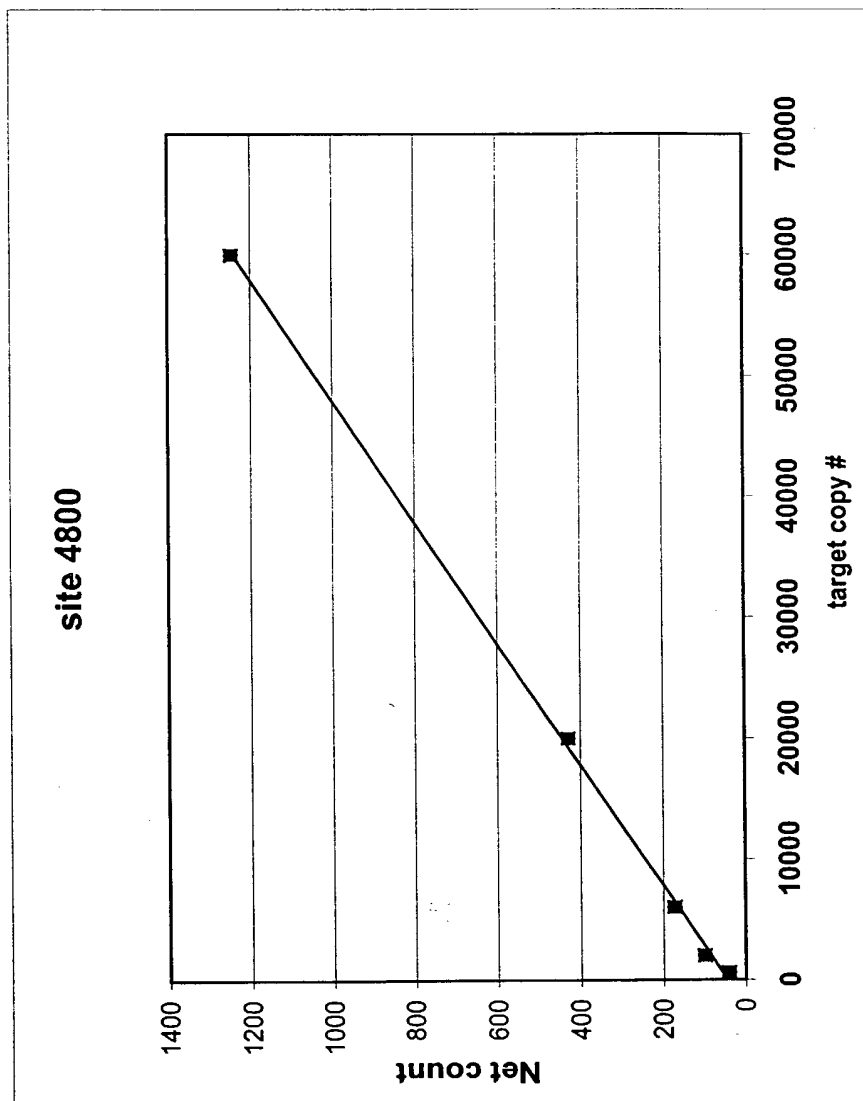
99/123

FIGURE 66



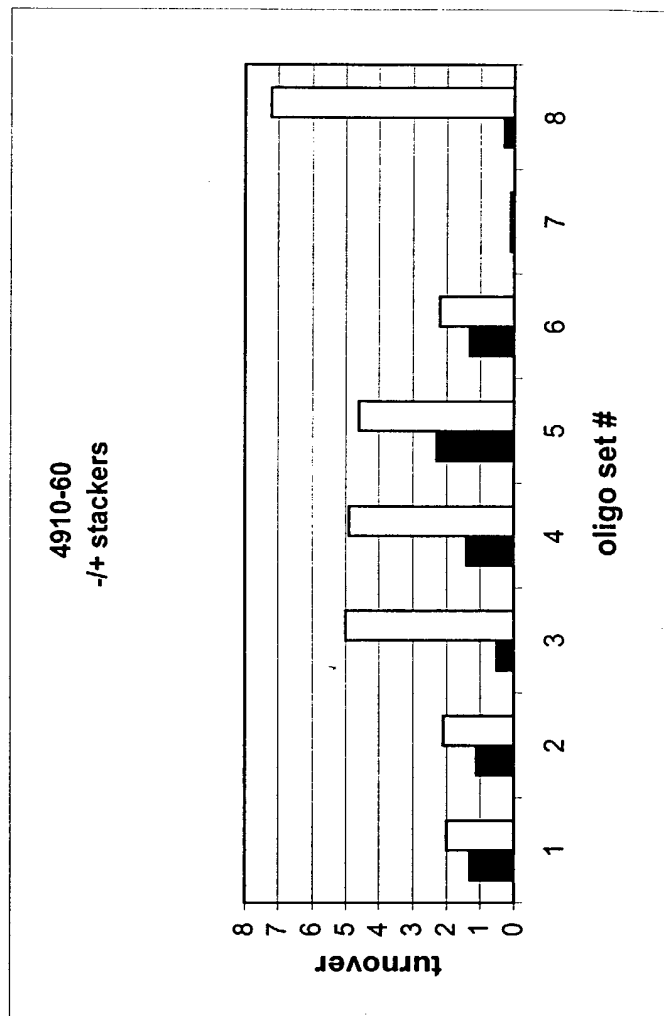
FOST90" 5462860

FIGURE 67



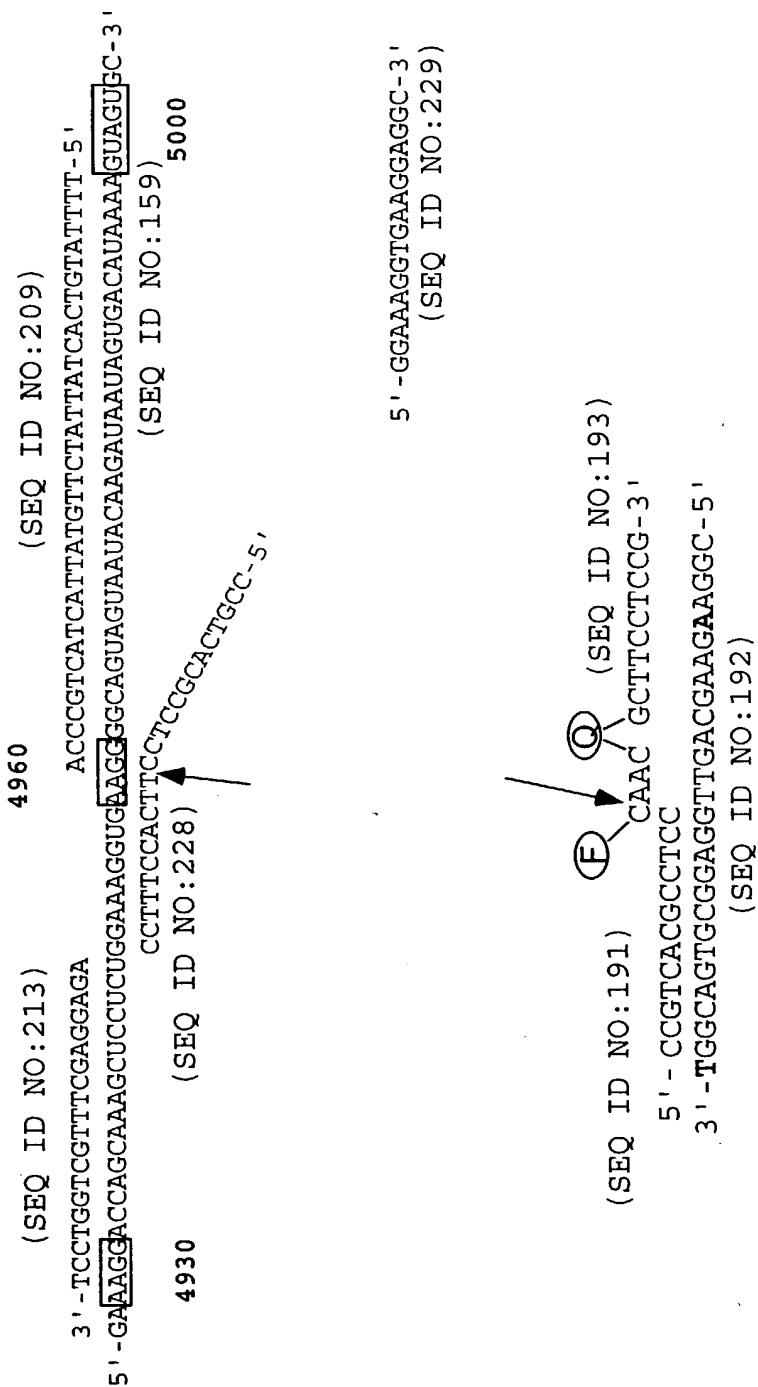
101/123

FIGURE 68



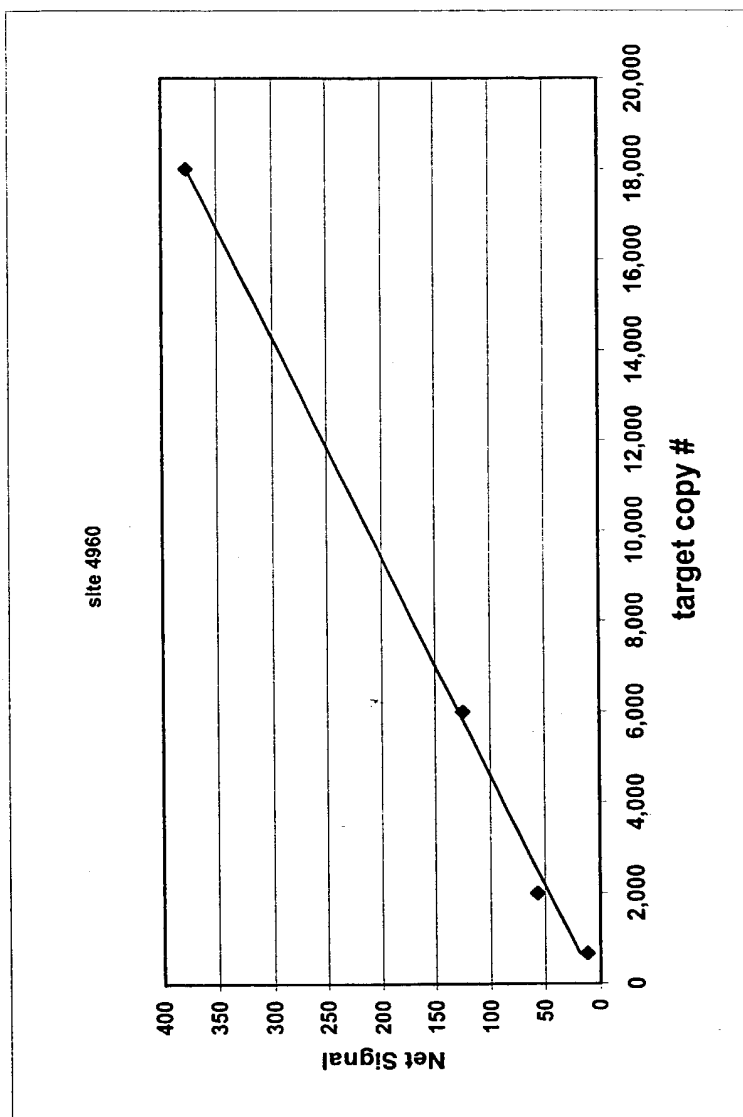
102/123

FIGURE 69



FOSTSD-51628860

FIGURE 70



104/123

FIGURE 71

Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGGGCAGCGUUGUGAUCUUUGCCACCUUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUUCAUACCUAUGAGGGAGUCCAGGAGAUUCAACCA
GGAA AUGCAUGGAUCUCAAGGAAACAAACACCCAAUAAACUCGGAGUGGCAGACUGAC
AACUGUGAGACAUGCACUUGCUACGAAACAGAAAUUUCAUGUUGCACCCUUGUUUCUAC
ACCUGUGGGUUAUGACAAAGACAACUGCCAAAGAAUCUUCAAGAAGGAGGACUGCAAGU
AUAUCGUGGUGGAGAAGAAGGACCCAAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUC³CCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA
AUAGUCA AUGAUUGUGUAGCCAUGCCUAUCAGUAAAAAGAUUUUUG

105/123

09882945-061501

FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)
520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAAUGCAGAUUUUCGUGAAAACCCUUA CGG GGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUA AAGGC CAAGAUC CAGGAUAAGGAAGGAU
UCCUCCUGACAGCAGAGACUGAUCUUUCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUCAUCUUGUGUUGAGACUU CGUGGUG G
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAA GCU GGCUGUCCUGAAAUAUUAUAAGGUGGAUGAGAAUGGCCAAAUAUAGUC
GCCUUCGUCGAGAGUGCCCUUCUGAUGAAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCCAAAUGUUGUCUGA

106/123

FIGURE 73

HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUC
UUGGAU[AAACCC]GCUCAAUGCCUGGAGAUUU[GGG]CGUG[CCC]CCGCAAGACUGCU[AGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

107/123

FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAU[CAACCC]GCUCAAUGCCUGGAGAUUU[GGG]CGUG[CCCC]CG[CG]AGACUGCU[AGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

108/123

0982945.061501

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)

898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)

898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)

898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCGGGAAGACUGGGUCCUUUC
UUGGAUAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUCGUAGACCGU[GCACCAUGAG]

109/123

0983945.061504
POSTED 04-06-2000

FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC
CUAGCCAUGGCGUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUCGCUGGGGUGACCGGGUCCUUUC
UUGGAA[CAACCC]GCUCAAUACCCAGAAAUUUGGGCGUG[CCCC]CGCGAGAUAC[UAGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

110/123

09882945.061501

FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

| | | |
|-----------|----------------------------------|-----------------|
| 726-38-01 | 5'-ACAAGGGAAGAGAGATGAGGAACCAG-3' | (SEQ ID NO:246) |
| 666-33-01 | 5'-TTTGCCTTCTCATCACCAATGG-3' | (SEQ ID NO:247) |
| 937-03-01 | 5'-TET- aaggggaagagagatgag-3' | (SEQ ID NO:248) |
| 937-03-02 | 5'-TET-aggagtttgcaagaaac-3' | (SEQ ID NO:249) |
| 937-03-03 | 5'-TET-ggtgctgtcctgg-3' | (SEQ ID NO:250) |
| 937-03-04 | 5'-TET-cagttttggatctttgatg-3' | (SEQ ID NO:251) |
| 937-03-05 | 5'-TET-aggacgctgagga-3' | (SEQ ID NO:252) |
| 937-03-06 | 5'-TET-aacaagtcaaatcttctatg-3' | (SEQ ID NO:253) |
| 937-03-07 | 5'-TET-caatactgcagatggag-3' | (SEQ ID NO:254) |
| 937-03-08 | 5'-TET-aagccaggtattgca-3' | (SEQ ID NO:255) |
| 937-03-09 | 5'-TET-ctattgtttctgcacaga-3' | (SEQ ID NO:256) |
| 937-03-10 | 5'-TET-aaatgaagaagaacatagga-3' | (SEQ ID NO:257) |
| 937-03-11 | 5'-TET-ggtcaagccatcaga-3' | (SEQ ID NO:258) |

111/132

098945 061501
T05T90 5463860

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA
GUUUGCAAGAAACAGGUGCUUAACACUAAUUCACCUCCUGAACAAAGAAAUAUGGGCUGU
GACCGGAAUCUGUGGGCUCAUCGUGGGCUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG
AGGUAUUCUAAUGCCA GUUGGAGACCUGCUUAUCCA GAAGACAAUUA AAAAGCAAGUUG
UCCUCGAAGAAGGUACAAUUGCUUUUAAAAUUGGGUAAAA CAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUUUGAUGUGCAAAA UCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAU
UUUGAACCUCACUAUCAGUUGGAA CAGAGGCUGACAACUUCACAGUUCUCAUCUGGC
UGUGGCAGCUGCAUCCC AUAUCUAUCAAAAUCAAUUUGUUCAAAUGAUCCUCAAUUCAC
UUAUUACAAGUCAAAAUCUUCUAUGUCCAAGUCAGAACUUUGAGAGAACUGUU AUGG
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACUACAGUUGGUCUG
UUUUAUCCUUACAACAUAUCUGCAGAUGGAGUUUAUAAAGUUUUCAAUGGAAAAGAUAA
CAUAAGUAAAGUUGCCAUAAUCGACACAUUAUAAAGGUAAAAGGAAUCUGUCCUAUUGGG
AAAGUCACUGCGACAUGAUUAAUGGUACAGAU GCA GCCUCAUUCACCUCUUUGUUGAG
AAAAGCCA GGUAUUGCAGUUCUUUUCUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCA UCC AAGG
CCUUUGCCUCUCCAGUUGAAAA CCGAGACAACUAUUGUUU CUGCACAGAAAAAUUAUC
UCAAAAAAUUGUACAUCUAUUGGUGUGCUAGACAUCAGCAAUGCAAAGAAGGGAGACC
UGUGUACAUUUCACUCCUCAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAACCCAAAUGAAGAAGACAUAGGACAUACUUGGAUAUUAACCUAUAA CUG
GAUUCACUUUACA AUUUGCAAAACGGCUGCAGGUCAACCUAUUGGUCAAGC CAUCAGAA
AAAAUUCAAGUAUUAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAAA

09882945.061501

112/123

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01 5'-ATGGGGTTTGTAAAGTTG-3' (SEQ ID NO:260)
 761-47-02 5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3' (SEQ ID NO:261)
 937-05-01 5'-TET- atgggggtttgttaaagtt-3' (SEQ ID NO:262)
 937-05-02 5'-TET- gaagacgacgagagg-3' (SEQ ID NO:263)
 937-05-03 5'-TET- ggatgatagtctcgtgtg-3' (SEQ ID NO:264)
 937-05-04 5'-TET- gctgcagcatattgta-3' (SEQ ID NO:265)
 937-05-05 5'-TET- ctgctatttggtatgca-3' (SEQ ID NO:266)
 937-05-06 5'-TET- gcagaagtacatcgga-3' (SEQ ID NO:267)
 937-05-07 5'-TET- gacatgatggaggaga-3' (SEQ ID NO:268)
 937-05-08 5'-TET- agaagaaggatcggg-3' (SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUGUUAAGUUGUUAAGAAUAAGGCUCACUUUAAGAGAUACCAAGUGAAAUU
 UAGAAAGACGACGAGAGGGUAAAACUGAUUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG
 AUAAAAUAAAUACAAACACCCAAAUAACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
 AUCAUUGUCAGAUUGCUUAUGCCCUGAUAGAGGGGGAUAUGAUAGUCUGCGCACGUUA
 UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCUGACAAAUUAUGCUGCAGCAU
 AUUGUACUGGCCUGCUGCUGGCCCGCAGGCUUCUCAAUAGGUUGGCAUGGACAAGAUC
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAGUGGAAAGCAUUGAUGGUCAG
 CCAGGUGCCUUCACCUGCUAAUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA
 AGUUUUUGGUGCCUGAAGGGAGCUGUGGAUGGAGGCUUGUCUAUCCCUCACAGUACCA
 AACGAUUCCUUGGUUAUGAUUCUGAAAGCAAGGAUUUAAUGCAGAAGUACAUCGGAAG
 CACAUCAUUGGCCAGAAUGUUGCAGAUUACAUGCGCUACUUAAUGGAAGAAGAUGAAGA
 UGCUUACAAGAAACAGUUCUCUCAAUACAUAAGAACAGCGUAACUCCAGACAUGAUGG
 AGGAGAUGUAUAAGAAAGCUCAUGCUGCUAUAACAGAGAAUCCAGUCUAUGAAAGAAG
 CCCAAGAAAGAAGUAAAAAGAGAGGUGGAACCGUCCAAAAUGUCCCUUGCUCAGAA
 GAAGGAUCGGGUAGCUAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
 AGAGCUAAACCCAGC

113/123

FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA

Oligonucleotides

| | | |
|-----------|---------------------------------|-----------------|
| 726-39-01 | 5'-GCTCAAGAATGTCCGCATAGACCCG-3' | (SEQ ID NO:271) |
| 666-34-01 | 5'-CTGGTCCCTGAGTTGTTTTTGC-3' | (SEQ ID NO:272) |
| 937-01-01 | 5'-TET- GCTCAAGAATGTCCG-3' | (SEQ ID NO:273) |
| 937-01-02 | 5'-TET- gggatgtggaaggag-3' | (SEQ ID NO:274) |
| 937-01-03 | 5'-TET- ggaccctatgtctacag-3' | (SEQ ID NO:275) |
| 937-01-04 | 5'-TET- acatcttggtcctgg-3' | (SEQ ID NO:276) |
| 937-01-05 | 5'-TET- tctcaacacgtacctc-3' | (SEQ ID NO:277) |
| 937-01-06 | 5'-TET- cggactcagcaaga-3' | (SEQ ID NO:278) |
| 937-01-07 | 5'-TET- caagggtgtttgaagg-3' | (SEQ ID NO:279) |
| 937-01-08 | 5'-TET- ctctgtttctctccca-3' | (SEQ ID NO:280) |
| 937-01-09 | 5'-TET- gtgaagatgcagctg-3' | (SEQ ID NO:281) |
| 937-01-10 | 5'-TET- agctggtgctgatg-3' | (SEQ ID NO:282) |
| 937-01-11 | 5'-TET- caggcctactctgag-3' | (SEQ ID NO:283) |
| 937-01-12 | 5'-TET- ggactctctcagcg-3' | (SEQ ID NO:284) |

0932345.061501

114/123

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUC
CCGUCCC UUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC[GAG]GUCCUC
AACGGCCAGAAGCCAGUAGU[CCGGG]AGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
AAAGGUCAACAUCACCUUCAUGA[CAACGACACC]GUGUCCUUCGUGGAGAA[CCGCAGC]C
UCCAUUUCCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA
UCUUGGUCCUGGGGGGCUCAUAUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
AUGACCUUGGCGCUGGUCACCAUGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUJUUCUCAACACGUACCUC CAGACAU
GCUUCCCAUAAAGGGCAAUUGGCCUGUUUGUUGGAUGAACAACUCGAAUUC[UGG]GG
UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG
AACGGACUCAGCAAGAUCGAUUAU[UGGCAUUCAGAGCA]GUGUAACAUGAUCAA[UGG]GAC
U[UCCGG]GCAGAUG[UGGGC]ACCCUUCA[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC
[CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU
CCCACGUAUCGCUUC[ACGGCC]CCCGAUACUCUGUUUGCCAACGGGUCCGUCUACCCACC
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU
UGGUGCGCCUCUGUUUCUCUCCACCCCCACUJUUAAC[AACGCCGAC]CCUGUGUUGUCAG
AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUCCUUGUCCUAGACAUCCA[U]
[CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCAGC]UGA[GCCUCUACAUCAA
AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU
GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU
GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAAUUCUUUUUGUUUUGGA
GUGGUAGUAAAAGGGCUCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCUGA
UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA
CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG
CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU
CACACCUGUCCGCACGCACGGCACAUGGAUGCCCACGCAUGUGCAAAAACAACUCAGGGA
CCAG

115/123

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

| | | |
|-----------|---|-----------------|
| 761-57-01 | 5'-taatacgactcactatagggacggaagtccaagagcatcactg-3' | (SEQ ID NO:286) |
| 761-57-03 | 5'-gcagggtacctggtccgta-3' | (SEQ ID NO:287) |
| 781-65-01 | 5'-TET-ggaagtccaagagca-3' | (SEQ ID NO:288) |
| 781-65-02 | 5'-TET-aatggcttctttggg-3' | (SEQ ID NO:289) |
| 781-65-03 | 5'-TET-ggcgtcgccc-3' | (SEQ ID NO:290) |
| 781-65-04 | 5'-TET-tacttccgcacgcgc-3' | (SEQ ID NO:291) |
| 781-65-05 | 5'-TET-cttcttccctagttgtg-3' | (SEQ ID NO:292) |
| 781-65-06 | 5'-TET-tgcctggccgt-3' | (SEQ ID NO:293) |
| 781-65-07 | 5'-TET-gactctactaagaaccca-3' | (SEQ ID NO:294) |
| 781-73-01 | 5'-TET-ccatcttagtggcgt-3' | (SEQ ID NO:295) |
| 781-73-02 | 5'-TET-caacaagtgccctgg-3' | (SEQ ID NO:296) |
| 781-85-01 | 5'-TET-aacacggcggtcac-3' | (SEQ ID NO:297) |
| 781-85-02 | 5'-TET-tgattacccccgagg-3' | (SEQ ID NO:298) |
| 781-85-03 | 5'-TET-acgctgttttcctg-3' | (SEQ ID NO:299) |
| 781-85-04 | 5'-TET-tgagacacctgtacaa-3' | (SEQ ID NO:300) |
| 781-85-05 | 5'-TET-gacggagacagtgg-3' | (SEQ ID NO:301) |
| 781-85-06 | 5'-TET-caagcgagggagag-3' | (SEQ ID NO:302) |

116/123

[illegible]

GGAAGUCCAAGAGCAUCACUGACAUCUUACCUCCUGAACCUGGGCCUUGAGCGACCCAGCUCUC
UUUGUGGGCCACUUUGCCCUUCUGGACUCACUACCUCUUCAGCCAUGAGGGCCUCCACAA
CGCCAUGUGCAAGCUCACGACUGCUUUCUUCUUCAUUUGGCUUCUUUGGGGGCAUAUUCU
UCAUCACCGUCAUCAGCAUCGACCGGUACCUCGCCAUCGUCCUGGCCGCCAACUCCAUG
AACAACCGGACAGUGCAACACGGCGUCACCAUCAGUCUGGGCGUCUGGGCGGCGGCCAU
CUUAGUGGCGUCGCCCCAGUUCAUGUUCACAAAGAGAAAGGACAACGAAUGUUUGGGUG
AUUACCCCGAGGUCCUGCAGGAAAUCUGGCCCGUGCUCCGCAACUCGGAGGUCAACAUC
CUGGGCUUCGUCUCCUGCCCUUGCUUAUCAUGAGCUUUUUGCUACUUCCGCAUCGUCCGGAC
GCUGUUUUCCUGCAAGAACC~~CGGAAGAAGGCCAGAGCCAUUAGGCUCAUCCUCUUGGUGGU~~
UGUUGUCUUCUCCUCUUCUGGACGCCUUAACAACAUCGUGAUUUUCCUGGAGACUCUCA
AAUUCUACAACUUCUUCUCCUAGUUGUGGCAUGAAGAGGGACCUGAGGUGGGCCCUUAGU
GUGACGGAGACAGUGGCGUUUAGCCACUGCUGCCUCAACCCCUUUAUCUACGCUUUCG
UGGGGAAAAGUUCAGAAGGUACUGAGACACCUGUACAACAAGUGCCUGGCCGUCUUGU
GCGGUCGUCCUGUCCACGCCGGCUUCUCAACAGAGUCCAGAGGAGCAGGCAGGACAGC
AUUCUGAGCAGCUUGACUCACUACACAAGCGAGGGAGAGGGAUCUCUCCUGCUCUGAAGG
GUCUCCCCGACCCCGACUCUACUAAGAACCCAGAGUCCUGCAUCUGACUCUGUGUAAG
AAAACAGAUUCACCCCG
CUCCUCCUGCAUUUUAUGUGCAAGAAAUACGGACCAGGUACCUGC

117/123

FIGURE 81A

Human Interleukin-1 beta (IL-1 β) Oligonucleotides

720-82-01 5'-
gtaatttaatacgaactcactataggggaaggtgcagttttgcccaaggagtgctaaag-3'
(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'
(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)

781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)

781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)

781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)

781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)

781-50-06 5'-TET-ccctagtctgctagc-3' (SEQ ID NO:311)

781-50-07 5'-TET-ttcaagtgtacttattaacc-3' (SEQ ID NO:312)

781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)

781-72-02 5'-TET-tgcagttttgccaaag-3' (SEQ ID NO:314)

0000045-001504

118/123

FIGURE 81B

Human Interleukin-1 beta (IL-1 β) (GenBank Accession #
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGA¹AAUGAUGGCUUAUUA²CAGUGGCAAUGAGG³AUG
ACUUGUUCUUUGAAG⁴CUGAUGGC⁵CCUAAACAGAUGAAGUGCUCCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCU⁶CCGACCAC⁷CACUA⁸CAGCAA⁹GGG
CUUCAGGCAGGCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUU¹⁰C
¹¹CCUGCC¹²CACAGACCUUCCAGGAGAAUGA¹³CCUG¹⁴AGCACCUCUUUCCCUUCAUCUUUGAA
GAAGAACCUAUCUUCUUCG¹⁵ACACAUGG¹⁶GAU¹⁷AACGA¹⁸GGCUUAUGUG¹⁹CACGA²⁰UGCACCUGU
²¹ACGAUC²²ACUGAACUGCACGCUCCG²³GGACUCACAGCAAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCU²⁴CUCC²⁵ACCUC²⁶CAGGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGUCCUUUGUACAAGGAGAAGAAAGUAAUGACAAAUAACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUAC²⁷CUGUCCUGCG²⁸UGUUGAAAGAUGAUAAAGCCCACUCUACAGCU
GGAGAGUGUAGAUC²⁹CCAAAAUUA³⁰CCCAAAGAAGAUGGAAAAGCGAUUUGUCUUCAA
CAAGAUAGAAUCAAU³¹AACAAGCU³²GGAAUUGAG³³UCUG³⁴CCCAGUCCCCAACUGGUAC³⁵A
³⁶UCAGCACCU³⁷UCUCAAGCAGAAAA³⁸CAUGC³⁹CCGUCUCCUGGGAGGGACCAAAG⁴⁰GCGG⁴¹CCAG
GAUAUAACUGACUUC⁴²ACCA⁴³UGCAAUUGUGUCUCCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAUCC⁴⁴CUAGGGCU⁴⁵GGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAUGCCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCA⁴⁶UCAGCCA⁴⁷GGACAGUCAGCUCUCUCCUUU⁴⁸CA⁴⁹
⁵⁰GGGCCAAUCC⁵¹CCAGC⁵²CCUUUUGUU⁵³GAGCCAGGCCUCUCUCAC⁵⁴CUCUCCUACUCACUU⁵⁵AA⁵⁶
⁵⁷AGCCCGCC⁵⁸UGACAGA⁵⁹AACCACGG⁶⁰CCACAUUGGUUCUAAGAAACCCUCUGUCAUUCGCU
CCCACAUUCUGAU⁶¹GAGCAACCGCU⁶²UCCCUAUUUUAUUUAUUUAUUUGUUUGUUUUUA
UUCAUUGGUCUAAUUUAUU⁶³CAAAGGGGGC⁶⁴AAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUUAAUAGCUAUGGAAUCAAUUCAAUUGGA⁶⁵CUG⁶⁶GUGUGCUCUCUUUAAAUCAAGU
CCUUUAA⁶⁷UUAAGAC⁶⁸UGAAAAUAU⁶⁹AUAAGCU⁷⁰CAGAUUAUUU⁷¹AAAUG⁷²GGAAUAUUUAUAA⁷³A
⁷⁴UGAGCAAUAUCAUACUGUUA

119/123

FIGURE 82A

Human Interferon gamma Oligonucleotides

| | | |
|-----------|--|-----------------|
| 448-59-01 | 5'-TET-GCATCGTTTTGGGTTCTCTT | (SEQ ID NO:316) |
| 448-59-02 | 5'-TET-ACTTTAAAGATGACCAGAGC | (SEQ ID NO:317) |
| 448-79-01 | CACATTGTTCTGATCATCTG | (SEQ ID NO:318) |
| 448-79-02 | CGGTAAGTGAATGTC | (SEQ ID NO:319) |
| 448-79-03 | TAGTAAGTGAATGTC | (SEQ ID NO:320) |
| 448-79-04 | GACATTCAAGTCAGTTACCG | (SEQ ID NO:321) |
| 498-20-01 | AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG | (SEQ ID NO:322) |
| 498-20-02 | AATTTAATACGACTCACTATACGGTAAGTGAATGTC | (SEQ ID NO:323) |
| 498-20-03 | 5'-TET-CACATTGTTCTGATCATCTG | (SEQ ID NO:324) |
| 498-20-04 | 5'-TET-CGGTAAGTGAATGTC | (SEQ ID NO:325) |
| 498-40-01 | 5'- AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA | (SEQ ID NO:326) |
| 498-40-02 | 5'- AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC | (SEQ ID NO:327) |
| 498-84-01 | 5'-TET-CATTCAGATGTAGCG | (SEQ ID NO:328) |
| 498-84-02 | 5'-TET-GACTCATCAATCAAA | (SEQ ID NO:329) |
| 498-84-03 | 5'-TET-GATTACAAGGCTTTA | (SEQ ID NO:330) |

120/123

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCaucugaAGAUcAGCUAUUAGAAGAGAAAGAUcAGUUAAGUCCUUU
GGACCUGAUcAGCUUGA[UACAA]GAACUACUGAUUUCAACUUCUUUGG[CUUAAU]UCUCUC
GGAAACGAUGAAAUAUACAAGUUUAUcUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUUACUGCCAGGACCCAUAUGUA[CAAGAAGC]AGAAAACCUUAAGAAAUAUU
UUAA[UGCAG]GUCAUUCAGAUG[UAGC]GGAUAAUGGAACUCUUUUUCUAGGCAUUUUGAAG
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUUG[CAGA]GCCAAAUUGUCUCCUUUUACUU
CAAACUUUUUAAAAACUUUAAAGA[UGACCAGA]GCAUC[CAAAAG]AGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUUCAAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGU[CGCCAG]CAGCUAAA[ACAGGGAAGCGAAAAAG]GAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCAGUAAUGGUUGUCCUGCCUACAAUAUUUGAAU
UUUAAAUCUAAAUCUAAUUUAUUAAUAUAACAUUAUUUAUAUGGGGAUAUAUUUUUAGAC
UCAUCAAUCAAUAAGUAUUUAUAAUAGCAACUUUUGUGUAAUGAAAAUGAAUAUCUAUU
AAUAUAUGUAUUUAUUUAUAAUCCUAUAUCCUGUGACUGUCUCACUUAUCCUUUGUUUU
CUGACUAAUUAG[GCAA]GGCUAUGUGAUU[ACAAG]GGCUUUUUC[UCAGGG]GCCAACUA[GGCA]
[GCCAACC]UAAG[CAAGA]UCCCAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAAUGAAC
ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

09882945.061501

121/123

FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION #
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAAUAAAUUCAGAUUGC
GACACUGUCAAAUUGC GGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAUAGCCCUGGGUAUAGUAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGA CUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUUUCUUGCAGUGCUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION #
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUCCAGAAAUGGGCCGCGGUGUUUUUGACCUGC
UAGUC GAUCUGGCCAGACGUUAUCUGUGGGUGGCCAGCGGCGACUAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCG UAGAG
CAGGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUAA GGUACGUGCCG UCCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

122/123

FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG
AUAAUACCGUUGUUUUUUUAGUGGGUAUUCUUUUACGCUUUCGUAGGAGCGAGUCCCAC
ACUCUUGGAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCCGGA
GCUCGCUCCCUUGGCUUCCCUUAUAUAUUUUAACAUCAGAAACAGACAUUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAUCUCGGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG

123/123

0982945-061501